GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 18:26:51 ; Search time 7218 Seconds
(without alignments)
11305.662 Million cell updates/sec

Title: US-10-023-782A-3
Perfect score: 2804
Sequence: 1 tcgcagagccgccgatgcgt.....gaaaaaaaaaaaaaaaaaaa 2804

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
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36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	30.4	1.1	49	6	AX099434	AX099434 Sequence
2	30	1.1	45	6	AX287571	AX287571 Sequence
3	30	1.1	45	6	AX287575	AX287575 Sequence
4	29.2	1.0	43	6	AX225198	AX225198 Sequence
5	29.2	1.0	50	6	AX261361	AX261361 Sequence
c 6	29.2	1.0	50	6	I36502	I36502 Sequence 1
7	29	1.0	46	6	AX287578	AX287578 Sequence
8	29	1.0	46	6	AX287582	AX287582 Sequence
c 9	28.8	1.0	45	6	E50989	E50989 Method for
c 10	28.4	1.0	40	6	A48799	A48799 Sequence 6
11	28.4	1.0	46	6	AX287579	AX287579 Sequence
12	28.4	1.0	46	6	AX287583	AX287583 Sequence
13	28	1.0	37	6	AX106972	AX106972 Sequence
c 14	28	1.0	37	6	I29931	I29931 Sequence 44
15	27.8	1.0	43	6	AX443022	AX443022 Sequence
16	27.8	1.0	43	6	AX459616	AX459616 Sequence
17	27.8	1.0	44	6	AX206861	AX206861 Sequence
c 18	27.6	1.0	44	6	AR038858	AR038858 Sequence
c 19	27.6	1.0	49	11	G73668	G73668 RZ220R etio
20	27.4	1.0	38	6	E50766	E50766 Vector expr
21	27.4	1.0	49	3	DDU63607	U63607 Dictyosteli
22	27.4	1.0	50	6	I23510	I23510 Sequence 5
23	27.4	1.0	50	6	I28359	I28359 Sequence 5
24	27.4	1.0	50	6	I28514	I28514 Sequence 5
25	27.4	1.0	50	6	I41125	I41125 Sequence 5
26	27.4	1.0	50	6	I49056	I49056 Sequence 5
27	27.4	1.0	50	6	I70295	I70295 Sequence 5
28	27.4	1.0	50	6	I90068	I90068 Sequence 5
29	27.2	1.0	33	6	BD011883	BD011883 Detection
30	27.2	1.0	33	23	BD004363	Bd004363 Detection
31	27.2	1.0	42	6	I32405	I32405 Sequence 2
32	27.2	1.0	47	6	AX458031	AX458031 Sequence
c 33	27.2	1.0	48	6	AX166869	AX166869 Sequence
c 34	26.8	1.0	44	6	I29927	I29927 Sequence 40
35	26.6	0.9	43	6	AX395321	AX395321 Sequence
36	26.4	0.9	43	6	AX484406	AX484406 Sequence
37	26.2	0.9	46	6	AX287577	AX287577 Sequence
38	26.2	0.9	46	6	AX287581	AX287581 Sequence
39	26.2	0.9	49	11	G73668	G73668 RZ220R etio
40	26	0.9	34	6	A63578	A63578 Sequence 19
41	26	0.9	45	6	AX287570	AX287570 Sequence
42	26	0.9	45	6	AX287574	AX287574 Sequence
43	25.8	0.9	48	6	AR020989	AR020989 Sequence
44	25.8	0.9	48	6	AR043404	AR043404 Sequence
45	25.8	0.9	48	6	AR062319	AR062319 Sequence

ALIGNMENTS

RESULT 1
AX099434/c
LOCUS AX099434 49 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 74 from Patent WO0119988.
ACCESSION AX099434
VERSION AX099434.1 GI:13538544
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 49)
AUTHORS Jacobs,K., Mccoy,J.M., Lavallie,E.R., Collins-Racie,L.A., Evans,C.,
Merberg,D., Treacy,M., Bowman,M.R., Spaulding,V. and Agostino,M.J.
TITLE Secreted proteins and polynucleotides encoding them

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  JOURNAL   Patent: WO 0119988-A 74 22-MAR-2001;
            Genetics Institute, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     misc_feature    1. .49
                     /note="n = A,T,C or G"
BASE COUNT       44 a      0 c      1 g      3 t      1 others
ORIGIN

  Query Match             1.1%;  Score 30.4;  DB 6;  Length 49;
  Best Local Similarity   75.5%;  Pred. No. 1.6e+05;
  Matches   37;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy   2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTTAACTTTGAAAGTT 2199
          ||  |||||||||   ||||||||||||||||||||   | |  || ||
Db     49 TTTTTTTTTTCTTTATTTTTTTTTTTTTTTTTTTTTTNTTTAATTT 1


RESULT 2
AX287571
LOCUS       AX287571                  45 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 14 from Patent WO0177390.
ACCESSION   AX287571
VERSION     AX287571.1  GI:17049337
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   abarz A,P.
  TITLE     Process for allele discrimation utilizing primer extension
  JOURNAL   Patent: WO 0177390-A 14 18-OCT-2001;
            Molecular Staging, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="P1 primer for use in allele discrimination"
BASE COUNT        1 a      6 c      0 g     38 t
ORIGIN

  Query Match             1.1%;  Score 30;  DB 6;  Length 45;
  Best Local Similarity   86.8%;  Pred. No. 1.9e+05;
  Matches   33;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy   2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          |||||||  |  |||||||||||||||||||| || ||
Db      4 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCACCTT 41


RESULT 3
AX287575
LOCUS       AX287575                  45 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 18 from Patent WO0177390.
ACCESSION   AX287575
VERSION     AX287575.1  GI:17049341
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   abarz A,P.
  TITLE     Process for allele discrimation utilizing primer extension
  JOURNAL   Patent: WO 0177390-A 18 18-OCT-2001;
            Molecular Staging, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="P1 primer for use in allele discrimination"
BASE COUNT        2 a      5 c      0 g     38 t
ORIGIN

  Query Match             1.1%;  Score 30;  DB 6;  Length 45;
  Best Local Similarity   86.8%;  Pred. No. 1.9e+05;
  Matches   33;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy   2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          |||||||  |  |||||||||||||||||||| || ||
Db      4 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCACCTT 41


RESULT 4
AX225198
LOCUS       AX225198                  43 bp    DNA     linear   PAT 10-SEP-2001
DEFINITION  Sequence 7 from Patent WO0161033.
ACCESSION   AX225198
VERSION     AX225198.1  GI:15555219
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Schouten,J.P.
  TITLE     Multiplex ligatable probe amplification
  JOURNAL   Patent: WO 0161033-A 7 23-AUG-2001;
            Schouten, Johannes Petrus (NL)
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="synthetic DNA"
BASE COUNT        0 a      0 c      0 g     43 t
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  Query Match             1.0%;  Score 29.2;  DB 6;  Length 43;
  Best Local Similarity   81.0%;  Pred. No. 2.6e+05;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy   2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          ||  |||||||  |  |||||||||||||||||||    |||
Db      1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42


RESULT 5
AX261361
LOCUS       AX261361                  50 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 1012 from Patent WO0173027.
ACCESSION   AX261361
VERSION     AX261361.1  GI:16510328
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Meagher,M.J., Xu,J. and King,G.E.
  TITLE     Compositions and methods for therapy and diagnosis of colon cancer
  JOURNAL   Patent: WO 0173027-A 1012 04-OCT-2001;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      0 c      0 g     50 t
ORIGIN

  Query Match             1.0%;  Score 29.2;  DB 6;  Length 50;
  Best Local Similarity   81.0%;  Pred. No. 2.7e+05;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy   2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          ||  |||||||  |  |||||||||||||||||||    |||
Db      1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42
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RESULT 6
I36502/c
LOCUS       I36502                    50 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 1 from patent US 5607834.
ACCESSION   I36502
VERSION     I36502.1  GI:2086327
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Bagwell,C.Bruce.
  TITLE     Fluorescent imperfect hairpin nucleic acid probes
  JOURNAL   Patent: US 5607834-A 1 04-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT       50 a      0 c      0 g      0 t
ORIGIN

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  Best Local Similarity   81.0%;  Pred. No. 2.7e+05;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy   2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
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Db     50 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 9


RESULT 7
AX287578
LOCUS       AX287578                  46 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 21 from Patent WO0177390.
ACCESSION   AX287578
VERSION     AX287578.1  GI:17049344
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   abarz A,P.
  TITLE     Process for allele discrimation utilizing primer extension
  JOURNAL   Patent: WO 0177390-A 21 18-OCT-2001;
            Molecular Staging, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="P1 primer for use in allele discrimination"
BASE COUNT        3 a      4 c      0 g     39 t
ORIGIN

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  Best Local Similarity   86.5%;  Pred. No. 2.9e+05;
  Matches   32;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy   2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTT 2191
           |||||||  |  |||||||||||||||||||| | ||
Db      1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCATTT 37


RESULT 8
AX287582
LOCUS       AX287582                  46 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 25 from Patent WO0177390.
ACCESSION   AX287582
VERSION     AX287582.1  GI:17049348
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   abarz A,P.
  TITLE     Process for allele discrimation utilizing primer extension
  JOURNAL   Patent: WO 0177390-A 25 18-OCT-2001;
            Molecular Staging, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="P1 primer for use in allele discrimination"
BASE COUNT        2 a      4 c      0 g     40 t
ORIGIN

  Query Match             1.0%;  Score 29;  DB 6;  Length 46;
  Best Local Similarity   86.5%;  Pred. No. 2.9e+05;
  Matches   32;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy   2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTT 2191
           |||||||  |  |||||||||||||||||||| | ||
Db      1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCATTT 37


RESULT 9
E50989/c
LOCUS       E50989                    45 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method for measuring nucleic acid and kit therefor.
ACCESSION   E50989
VERSION     E50989.1  GI:18622166
KEYWORDS    JP 2000300267-A/3.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Fujimura,K.
  TITLE     Method for measuring nucleic acid and kit therefor
  JOURNAL   Patent: JP 2000300267-A 3 31-OCT-2000;
            GIJUTSU KENKYU KUMIAI IRYO FUKUSHI KIKI KENKYUSHO
COMMENT     OS   Artificial Sequence
            PN   JP 2000300267-A/3
            PD   31-OCT-2000
            PF   21-APR-1999 JP 1999113165
            PR
            PI   KATSUYA FUJIMURA
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .45
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT       40 a      4 c      1 g      0 t
ORIGIN

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  Best Local Similarity   82.5%;  Pred. No. 3.1e+05;
  Matches   33;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy   2153 GATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
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Db     41 GTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT 10
A48799/c
LOCUS       A48799                    40 bp    DNA     linear   PAT 07-MAR-1997
DEFINITION  Sequence 6 from Patent WO9603528.
ACCESSION   A48799
VERSION     A48799.1  GI:2302466
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
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            unclassified.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Petrik,J., Allain,J. and Pearson,G.J.
  TITLE     OLIGONUCLEOTIDES AND THEIR USE
  JOURNAL   Patent: WO 9603528-A 6 08-FEB-1996;
            LYNXVALE LTD (GB)
COMMENT     Other publication AU 3118395 960222.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT       40 a      0 c      0 g      0 t
ORIGIN

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  Best Local Similarity   84.2%;  Pred. No. 3.7e+05;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          ||||||| |  ||||||||||||||||||||   |||
Db     40 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 3


RESULT 11
AX287579
LOCUS       AX287579                 46 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 22 from Patent WO0177390.
ACCESSION   AX287579
VERSION     AX287579.1  GI:17049345
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   abarz A,P.
  TITLE     Process for allele discrimation utilizing primer extension
  JOURNAL   Patent: WO 0177390-A 22 18-OCT-2001;
            Molecular Staging, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .46
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                     /db_xref="taxon:32630"
                     /note="P1 primer for use in allele discrimination"
BASE COUNT        2 a      3 c      0 g     41 t
ORIGIN

  Query Match             1.0%;  Score 28.4;  DB 6;  Length 46;
  Best Local Similarity   84.2%;  Pred. No. 3.7e+05;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          ||||||| |  ||||||||||||||||||||   || |
Db      4 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTAT 41


RESULT 12
AX287583
LOCUS       AX287583                 46 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 26 from Patent WO0177390.
ACCESSION   AX287583
VERSION     AX287583.1  GI:17049349
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   abarz A,P.
  TITLE     Process for allele discrimation utilizing primer extension
  JOURNAL   Patent: WO 0177390-A 26 18-OCT-2001;
            Molecular Staging, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="P1 primer for use in allele discrimination"
BASE COUNT        1 a      3 c      0 g     42 t
ORIGIN

  Query Match             1.0%;  Score 28.4;  DB 6;  Length 46;
  Best Local Similarity   84.2%;  Pred. No. 3.7e+05;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          ||||||| |  ||||||||||||||||||||   || |
Db      4 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTAT 41


RESULT 13
AX106972
LOCUS       AX106972                 37 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 25 from Patent WO0125442.
ACCESSION   AX106972
VERSION     AX106972.1  GI:13922521
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Blanco,D.L., bernad Miana,A., dominguez Lopez,O. and garcia Diaz,M.
  TITLE     Dna polymerase lambda and uses thereof
  JOURNAL   Patent: WO 0125442-A 25 12-APR-2001;
            CONSEJO SUPERIOR. DE INVESTIGACIONES CIENTIFICAS (ES)
FEATURES             Location/Qualifiers
     source          1. .37
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                     /db_xref="taxon:32630"
                     /note="poly dT"
BASE COUNT        0 a      0 c      0 g     37 t
ORIGIN

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  Best Local Similarity   86.1%;  Pred. No. 4.3e+05;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy   2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
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Db      1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 36


RESULT 14
I29931/c
LOCUS       I29931                   37 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 44 from patent US 5578468.
ACCESSION   I29931
VERSION     I29931.1  GI:1820722
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Pickup,D.J., Patel,D. and Antczak,J.B.
  TITLE     Site-specific RNA cleavage
  JOURNAL   Patent: US 5578468-A 44 26-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .37
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BASE COUNT       36 a      1 c      0 g      0 t
ORIGIN

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  Best Local Similarity   86.1%;  Pred. No. 4.3e+05;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy   2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
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RESULT 15
AX443022
LOCUS       AX443022                43 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 1485 from Patent WO0214361.
ACCESSION   AX443022
VERSION     AX443022.1  GI:21690510
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Raitano,A.B., Challita-Eid,P.M., Faris,M., Saffran,D.C., Afar,D.E.,
            Levin,E., Hubert,R.S., Ge,W. and Jakobovits,A.
  TITLE     Nucleic acids and corresponding proteins entitled 83p2h3 and
            catrf2el1 useful in treatment and detection of cancer
  JOURNAL   Patent: WO 0214361-A 1485 21-FEB-2002;
            Agensys, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .43
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                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
BASE COUNT        3 a      2 c      2 g     36 t
ORIGIN

  Query Match             1.0%;  Score 27.8;  DB 6;  Length 43;
  Best Local Similarity   82.1%;  Pred. No. 4.7e+05;
  Matches   32;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy    2148 TGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
           ||||  |  ||||| |  ||||||||||||||||||||
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Search completed: March  3, 2003, 21:30:06
Job time : 7225 secs
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GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 17:59:45 ; Search time 595 Seconds
(without alignments)
10612.779 Million cell updates/sec

Title: US-10-023-782A-3
Perfect score: 2804
Sequence: 1 tcgcagagccgccgatgcgt.....gaaaaaaaaaaaaaaaaaaa 2804

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	31.4	1.1	47	22	AAL07489	Human reproductive
c	2	31.4	1.1	50	22	AAL28562	Human SNP oligonuc
	3	30.6	1.1	48	16	AAT04081	Trypsin inhibitory
c	4	30.4	1.1	49	19	AAV41447	Nucleotide sequenc
c	5	30.4	1.1	49	22	AAF98419	Human cDNA clone B
	6	30	1.1	45	24	AAS95724	Allele discriminat
	7	30	1.1	45	24	AAS95728	Allele discriminat
c	8	29.8	1.1	50	24	ABK30194	CYP2D6 gene polymo
	9	29.6	1.1	50	19	AAV37933	Primer of the spec
	10	29.2	1.0	43	22	AAD17216	Human mRNA hybridi
c	11	29.2	1.0	44	19	AAV09273	Nucleotide sequenc
c	12	29.2	1.0	49	18	AAT88080	3' portion of cDNA
c	13	29.2	1.0	49	18	AAV02146	Human secreted pro
c	14	29.2	1.0	50	15	AAQ66922	Poly-dA 50mer prob
c	15	29.2	1.0	50	22	AAF60897	Conjugate forming
	16	29.2	1.0	50	23	AAS58336	cDNA #1012 encodin
	17	29.2	1.0	50	24	ABN89414	Polymorphism detec
c	18	29	1.0	38	22	AAL07488	Human reproductive
	19	29	1.0	46	24	AAS95731	Allele discriminat
	20	29	1.0	46	24	AAS95735	Allele discriminat
c	21	28.8	1.0	43	22	AAL31948	Human SNP oligonuc
c	22	28.8	1.0	45	22	AAF26960	Primer for amplify
	23	28.4	1.0	40	13	AAQ25031	Oligonucleotide sp
	24	28.4	1.0	40	21	AAA39649	Primer used in con
	25	28.4	1.0	46	24	AAS95732	Allele discriminat
	26	28.4	1.0	46	24	AAS95736	Allele discriminat
c	27	28.2	1.0	36	24	AAD27117	RNA template, AU u
c	28	28.2	1.0	37	24	AAD27125	RNA template, (AU)
c	29	28.2	1.0	47	24	ABK30186	CYP2D6 gene polymo
c	30	28	1.0	44	22	AAL30581	Human SNP oligonuc
	31	28	1.0	48	22	AAS04299	Example PCR primer
c	32	28	1.0	49	18	AAT80510	Hepatoma AS-30D Ty
	33	27.8	1.0	42	21	AAA37946	DNA synthesis prim
	34	27.8	1.0	43	21	AAA09164	cDNA synthesis pri
	35	27.8	1.0	43	21	AAA14804	Oligonucleotide DP
	36	27.8	1.0	43	21	AAZ93041	Primer used for ge
	37	27.8	1.0	43	21	AAZ94895	cDNA synthesis pri
	38	27.8	1.0	43	21	AAZ94401	cDNA synthesis pri
	39	27.8	1.0	43	22	AAD06225	Human SGP28 cDNA s
	40	27.8	1.0	43	22	AAF76005	RT primer, SEQ ID
	41	27.8	1.0	43	22	AAD04804	Human secreted tum
	42	27.8	1.0	43	24	ABK67415	Human 83P2H3 cDNA
	43	27.8	1.0	43	24	ABL50400	Human 158P1H4 cDNA
	44	27.8	1.0	43	24	ABL50412	Human 158P1F4 cDNA
	45	27.8	1.0	43	24	AAS99436	DPNCDN cDNA synthe

ALIGNMENTS

RESULT 1
AAL07489/c
ID AAL07489 standard; DNA; 47 BP.
XX
AC AAL07489;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 10177.
XX
KW Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200155320-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01339.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
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PR 14-AUG-2000; 2000US-0225266.
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PR 22-AUG-2000; 2000US-0227182.
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PR 30-AUG-2000; 2000US-0228924.
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PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
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PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
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PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
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PR 21-SEP-2000; 2000US-0234223.
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PR 01-NOV-2000; 2000US-0244617.
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PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465570/50.
XX
PT Isolated nucleic acid molecule encoding a reproductive system antigen
PT is used in preventing, treating or ameliorating a medical condition -
XX
PS Disclosure; SEQ ID NO 10177; 1297pp + Sequence Listing; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a genomic sequence encoding a
CC protein of the invention.
XX
SQ Sequence 47 BP; 36 A; 4 C; 2 G; 5 T; 0 other;

Query Match 1.1%; Score 31.4; DB 22; Length 47;

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  Best Local Similarity   85.4%;  Pred. No. 2.1e+03;
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          | ||||  |||||||  |  ||||||||||||||||||||
Db     46 CAGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTA 6


RESULT 2
AAL28562/c
ID   AAL28562 standard; DNA; 50 BP.
XX
AC   AAL28562;
XX
DT   24-JAN-2002  (first entry)
XX
DE   Human SNP oligonucleotide #1770.
XX
KW   Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW   neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW   amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW   cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW   complement related protein; cytochrome; kinesin; cytokine; interferon;
KW   interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW   multifactorial disease; autoimmune disease; infection;
KW   nervous system disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200147944-A2.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US35498.
XX
PR   28-DEC-1999;   99US-0173419.
PR   27-DEC-2000; 2000US-0173419.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
DR   WPI; 2001-465210/50.
XX
PT   Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT   oncogenes and histones, useful for diagnosing and treating, e.g.
PT   cancer, autoimmune diseases and infections -
XX
PS   Claim 1; Page 1886; 4143pp; English.
XX
CC   The present invention relates to oligonucleotides encoding polymorphic
CC   variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC   apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC   histones, kinases, colony stimulating factors, complement related
CC   proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC   G-protein coupled receptors and thioesterases. The present sequence is
CC   one such oligonucleotide. The oligonucleotides and the peptides encoded
CC   by them may be used in the prevention, diagnosis and treatment of
CC   diseases associated with inappropriate expression of the proteins listed
CC   above. Disorders that may be prevented, diagnosed and/or treated include
CC   multifactorial diseases with a genetic component, such as autoimmune
CC   diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC   systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC   (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC   leukaemia), diseases of the nervous system and an infection of pathogenic
CC   organisms.
XX
SQ   Sequence 50 BP; 37 A; 9 C; 1 G; 3 T; 0 other;

  Query Match             1.1%;  Score 31.4;  DB 22;  Length 50;
  Best Local Similarity   77.6%;  Pred. No. 2.1e+03;
  Matches   38;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy   2145 TGCTGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTTG 2193
          || || ||  ||||||  |  |  |||||||||||||||||||||| |
Db     49 TGGTGTTTTTTTTTTTGTTGTTGGTTTTTTTTTTTTTTTTTTAACTTGG 1


RESULT 3
AAT04081
ID   AAT04081 standard; DNA; 48 BP.
XX
AC   AAT04081;
XX
DT   16-MAY-1996  (first entry)
XX
DE   Trypsin inhibitory protein cDNA antisense primer-1.
XX
KW   Trypsin; inhibitor; human T98G cells; pancreatitis; shock; DIC;
KW   multiple organ failure; disseminated intravascular coagulation; ss.
XX
OS   Synthetic.
XX
PN   JP07242700-A.
XX
PD   19-SEP-1995.
XX
PF   04-MAR-1994;   94JP-0059906.
XX
PR   04-MAR-1994;   94JP-0059906.
XX
PA   (MOCH ) MOCHIDA PHARM CO LTD.
XX
DR   WPI; 1995-355285/46.
XX
PT   Polypeptide having trypsin inhibitory activity - for the treatment
PT   of pancreatitis, shock, multi-organ failure, etc.
XX
PS   Example 7; Page 15; 25pp; Japanese.
XX
CC   A polypeptide having trypsin inhibitory activity, mol.wt. 22-28 kD
CC   or 17-23 kD (as determined by SDS-PAGE under reducing or non-
CC   reducing conditions, respectively) and an N-terminal sequence as in
CC   AAR79913 is claimed. The polypeptide was isolated from human T98G
CC   cells and is useful for treating pancreatitis, shock, multiple
CC   organ failure and disseminated intravascular coagulation. The
CC   present sequence is that of an antisense primer used for cloning
CC   T98G cDNA coding for the full-length polypeptide.
XX
SQ   Sequence 48 BP; 2 A; 1 C; 1 G; 44 T; 0 other;

  Query Match             1.1%;  Score 30.6;  DB 16;  Length 48;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   36;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   2148 TGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          ||| |  |||||||  |  |||||||||||||||||||||   |||
Db      2 TGAATTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 46


RESULT 4
AAV41447/c
ID   AAV41447 standard; cDNA; 49 BP.
XX
AC   AAV41447;
XX
DT   12-OCT-1998  (first entry)
XX
DE   Nucleotide sequence of the 3' portion of the BD176_3 clone.
XX
KW   Clone BD176_3; secreted protein; human cell; immuno-modulator; PCR;
KW   anti-tumour agent; tissue growth promoter; haemostatic agent; primer;
KW   thrombolytic agent; molecular weight marker; genetic disorder;
KW   antibody; ds.
XX
OS   Homo sapiens.
```

XX
PN WO9821332-A2.
XX
PD 22-MAY-1998.
XX
PF 14-NOV-1997; 97WO-US20740.
XX
PR 13-NOV-1997; 97US-0969515.
PR 15-NOV-1996; 96US-0749745.
PR 02-JUN-1997; 97US-0867678.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
PI Racie LA, Spaulding V, Treacy M;
XX
DR WPI; 1998-297936/26.
XX
PT New nucleic acid encoding secreted protein from human cells -
PT potentially useful, e.g. as immuno-modulators, anti-tumour agents,
PT promoters of tissue growth, haemostatic and thrombolytic agents
XX
PS Claim 24; Page 71; 98pp; English.
XX
CC This is the nucleotide sequence of the clone BD176_3, used in the
CC method of the invention involving secreted proteins from human cells
CC potentially useful as immuno-modulators, anti-tumour agents, tissue
CC growth promoters, haemostatic and thrombolytic agents. It was isolated
CC from a foetal human kidney cDNA library. They may be used to express
CC the recombinant protein, as tissue/molecular weight markers, for
CC chromosome identification, to identify possible genetic disorders and
CC isolate new related DNA, as sources of primers for PCR, to generate
CC anti-protein or anti-DNA antibodies, or in interaction trap assays to
CC identify sequences that encode interacting proteins.
XX
SQ Sequence 49 BP; 44 A; 0 C; 1 G; 3 T; 1 other;

Query Match 1.1%; Score 30.4; DB 19; Length 49;
Best Local Similarity 75.5%; Pred. No. 3.4e+03;
Matches 37; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTTAACTTTGAAAGTT 2199
|| ||||||||| |||||||||||||||||||| | | || ||
Db 49 TTTTTTTTTTCTTTATTTTTTTTTTTTTTTTTTTTTTTNTTTAATTT 1

RESULT 5
AAF98419/c
ID AAF98419 standard; cDNA; 49 BP.
XX
AC AAF98419;
XX
DT 07-JUN-2001 (first entry)
XX
DE Human cDNA clone BD176_3 3' sequence SEQ ID 74.
XX
KW Human; secreted protein; nutrient; cytokine modulator; proliferation;
KW differentiation; immune system modulator; tissue growth; chemotactic;
KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;
KW haematopoiesis.
XX
OS Homo sapiens.
XX
PN WO200119988-A1.
XX
PD 22-MAR-2001.
XX
PF 14-SEP-2000; 2000WO-US25135.
XX
PR 17-SEP-1999; 99US-0398829.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;
XX
DR WPI; 2001-244801/25.
XX
PT Isolated nucleic acids encoding polypeptides, useful for modulating
PT e.g. cytokine and cell proliferation/differentiation activity, the
PT immune system and hematopoiesis regulating activity -
XX
PS Disclosure; Page 429; 557pp; English.
XX
CC Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
CC proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
CC tissue types, and may be used in the prevention, treatment and diagnosis
CC of diseases associated with inappropriate protein expression. The
CC polypeptides and nucleic acids may be used as nutrients or to modulate
CC cytokine and cell proliferation/differentiation activity and may also be
CC involved in modulation of the immune system. The cDNA sequences,
CC proteins, their agonists and/or antagonists exhibit haematopoiesis
CC regulating activity; tissue growth activity; activin/inhibin activity;
CC chemotactic/chemokinetic activity; haemostatic and thrombolytic
CC activity; receptor/ligand activity; anti-inflammatory activity;
CC haematopoiesis activity; cadherin/tumour suppressor activity; and/or
CC tumour inhibition activity. Included in the invention are probes
CC represented in AAF98490 - AAF98572 which are specific for the cDNA clones
CC encoding the secreted proteins.
XX
SQ Sequence 49 BP; 44 A; 0 C; 1 G; 3 T; 1 other;

Query Match 1.1%; Score 30.4; DB 22; Length 49;
Best Local Similarity 75.5%; Pred. No. 3.4e+03;
Matches 37; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTTAACTTTGAAAGTT 2199
|| ||||||||| |||||||||||||||||||| | | || ||
Db 49 TTTTTTTTTTCTTTATTTTTTTTTTTTTTTTTTTTTTTNTTTAATTT 1

RESULT 6
AAS95724
ID AAS95724 standard; DNA; 45 BP.
XX
AC AAS95724;
XX
DT 14-FEB-2002 (first entry)
XX
DE Allele discrimination P1 primer #8.
XX
KW Rolling circle amplification; single nucleotide polymorphism; anaemia;
KW exonuclease deficient DNA polymerase; amplification target circle; RCA;
KW Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss;
KW Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis;
KW diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach;
KW lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma;
KW melanoma; PCR primer; sequencing primer; probe.
XX
OS Homo sapiens.
XX
PN WO200177390-A2.
XX
PD 18-OCT-2001.
XX
PF 05-APR-2001; 2001WO-US11151.
XX
PR 05-APR-2000; 2000US-194843P.
XX
PA (MOLE-) MOLECULAR STAGING INC.
XX
PI Abarzua P;
XX
DR WPI; 2002-049157/06.
XX
PT Detecting single nucleotide polymorphism involves amplifying target

PT sequences using small primer probe that matches or mismatches to target
PT sequence and extending primer probe which is then detected -
XX
PS Claim 15; Page 41; 67pp; English.
XX
CC The invention relates to detecting single nucleotide polymorphisms by
CC contacting an allele-specific oligonucleotide primer (P1) with a target
CC polynucleotide to form a hybridisation complex, where the target sequence
CC is complementary to P1 at one end but the terminal nucleotide and the
CC third nucleotide from the terminal at the other end of P1 may not be
CC complementary. The complex is then contacted with an exonuclease
CC deficient DNA polymerase enzyme under conditions that promote extension
CC of P1 with the target DNA as the template, thereby forming an extended
CC segment of P1. Oligonucleotide probes hybridising to one or more target
CC polynucleotides distinguish between matched and mismatched 3' ends, hence
CC the absence of sequence amplification indicates the presence of a single
CC nucleotide mismatch. Primer sequences complementary to a sequence on an
CC amplification target circle can be used in rolling circle amplification
CC (RCA). The method is useful for diagnosing a disease caused by, induced
CC by or related to a mutation in at least one gene, such as Parkinson's
CC disease, polycystic kidney disease, Tay-Sachs disease, Huntington
CC disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes,
CC obesity, cancers of the head, neck, skin, brain, oesophagus, stomach,
CC lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma and
CC melanoma. Sequences AAS95711-AAS95745 represent primers, targets and
CC fluorescence decorators used in the detection of RCA products.
XX
SQ Sequence 45 BP; 1 A; 6 C; 0 G; 38 T; 0 other;

Query Match 1.1%; Score 30; DB 24; Length 45;
Best Local Similarity 86.8%; Pred. No. 4e+03;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy    2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
           ||||||| |  |||||||||||||||||||| || ||
Db       4 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCACCTT 41
```

RESULT 7
AAS95728
ID AAS95728 standard; DNA; 45 BP.
XX
AC AAS95728;
XX
DT 14-FEB-2002 (first entry)
XX
DE Allele discrimination P1 primer #12.
XX
KW Rolling circle amplification; single nucleotide polymorphism; anaemia;
KW exonuclease deficient DNA polymerase; amplification target circle; RCA;
KW Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss;
KW Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis;
KW diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach;
KW lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma;
KW melanoma; PCR primer; sequencing primer; probe.
XX
OS Homo sapiens.
XX
PN WO200177390-A2.
XX
PD 18-OCT-2001.
XX
PF 05-APR-2001; 2001WO-US11151.
XX
PR 05-APR-2000; 2000US-194843P.
XX
PA (MOLE-) MOLECULAR STAGING INC.
XX
PI Abarzua P;
XX
DR WPI; 2002-049157/06.
XX
PT Detecting single nucleotide polymorphism involves amplifying target

PT sequences using small primer probe that matches or mismatches to target
PT sequence and extending primer probe which is then detected -
XX
PS Claim 15; Page 41; 67pp; English.
XX
CC The invention relates to detecting single nucleotide polymorphisms by
CC contacting an allele-specific oligonucleotide primer (P1) with a target
CC polynucleotide to form a hybridisation complex, where the target sequence
CC is complementary to P1 at one end but the terminal nucleotide and the
CC third nucleotide from the terminal at the other end of P1 may not be
CC complementary. The complex is then contacted with an exonuclease
CC deficient DNA polymerase enzyme under conditions that promote extension
CC of P1 with the target DNA as the template, thereby forming an extended
CC segment of P1. Oligonucleotide probes hybridising to one or more target
CC polynucleotides distinguish between matched and mismatched 3' ends, hence
CC the absence of sequence amplification indicates the presence of a single
CC nucleotide mismatch. Primer sequences complementary to a sequence on an
CC amplification target circle can be used in rolling circle amplification
CC (RCA). The method is useful for diagnosing a disease caused by, induced
CC by or related to a mutation in at least one gene, such as Parkinson's
CC disease, polycystic kidney disease, Tay-Sachs disease, Huntington
CC disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes,
CC obesity, cancers of the head, neck, skin, brain, oesophagus, stomach,
CC lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma and
CC melanoma. Sequences AAS95711-AAS95745 represent primers, targets and
CC fluorescence decorators used in the detection of RCA products.
XX
SQ Sequence 45 BP; 2 A; 5 C; 0 G; 38 T; 0 other;

Query Match 1.1%; Score 30; DB 24; Length 45;
Best Local Similarity 86.8%; Pred. No. 4e+03;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy    2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
           ||||||| |  |||||||||||||||||||| || ||
Db       4 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCACCTT 41
```

RESULT 8
ABK30194/c
ID ABK30194 standard; DNA; 50 BP.
XX
AC ABK30194;
XX
DT 23-APR-2002 (first entry)
XX
DE CYP2D6 gene polymorphism detection primer #33.
XX
KW Human; CYP2D6; primer; single nucleotide polymorphism detection; SNP;
KW ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200196604-A2.
XX
PD 20-DEC-2001.
XX
PF 11-JUN-2001; 2001WO-US18912.
XX
PR 12-JUN-2000; 2000US-210988P.
XX
PA (GENI-) GENICON SCI CORP.
XX
PI Bee G, Kohne DE, Korb L, Peterson T, Yguerabide J;
XX
DR WPI; 2002-130745/17.
XX
PT Determining the presence of a CYP2D6 target sequence in a DNA sample
PT containing CYP2D6 nucleic acid, for detecting mutations or
PT polymorphisms, comprises detecting the scattered light from a particle
PT bound to the target sequence -
XX

```
PS   Example 2; Figure 6; 66pp; English.
XX
CC   The invention relates to a method of determining the presence or absence
CC   of a CYP2D6 target sequence in a DNA sample containing CYP2D6 nucleic
CC   acid. Determining the presence or absence of a CYP2D6 target sequence in
CC   a sample of DNA containing CYP2D6 nucleic acid comprises contacting the
CC   nucleic acid with a probe under stringent binding conditions, and
CC   detecting the presence or absence of the target sequence bound with the
CC   probe with a scattered light detectable particle, by observing light
CC   scattered from the particle which indicates the presence of the target
CC   sequence. The method is useful for determining the presence or
CC   absence of particular single nucleotide polymorphisms or alleles in
CC   genomic nucleic acid, especially in a pharmacogenetically relevant gene
CC   or genes in a DNA sample, and to detect and measure one or more target
CC   sequences in a sample. The method may also be used to detect specific
CC   mutations to identify the phenotypic classification of an individual.
CC   ABK30162-ABK30230 represent CYP2D6 target sequence-specific primers
CC   of the invention.
XX
SQ   Sequence 50 BP; 36 A; 1 C; 10 G; 3 T; 0 other;

  Query Match             1.1%;  Score 29.8;  DB 24;  Length 50;
  Best Local Similarity   75.5%;  Pred. No. 4.6e+03;
  Matches   37;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy    2157 TTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTTGAAAGTTAACTCT 2205
           ||||| |  |||||||||||||||||||| ||| | |     | ||||
Db      50 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTCACTCTCACCTCCATCTCT 2

RESULT 9
AAV37933
ID   AAV37933 standard; cDNA; 50 BP.
XX
AC   AAV37933;
XX
DT   05-OCT-1998  (first entry)
XX
DE   Primer of the specification.
XX
KW   Leukocyte; IgA nephropathy; diagnosis; treatment; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9824815-A1.
XX
PD   11-JUN-1998.
XX
PF   05-DEC-1997;   97WO-JP04469.
XX
PR   05-DEC-1996;   96JP-0325752.
XX
PA   (KAZU-) KAZUSA DNA RES INST FOUND.
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Ishiwata T,  Kuga T,  Nagase T,  Nakagawa S,  Nishi T;
PI   Nishimura A,  Nomura N,  Sakurada M,  Sawada S,  Takei M;
XX
DR   WPI; 1998-333259/29.
XX
PT   Protein from leukocytes and DNA encoding it - useful as reagents for
PT   diagnosing and treating IgA nephropathy
XX
PS   Example 1; Page 33; 41pp; Japanese.
XX
CC   PCR primers AAV37933-39 are used in the course of the invention. The
CC   specification descibes a novel protein isolated from leukocytes of
CC   patients with IgA nephropathy. Oligonucleotides based on the DNA
CC   sequence encoding this protein are useful as reagents for diagnosing
CC   and treating IgA nephropathy.
XX
SQ   Sequence 50 BP; 2 A; 6 C; 6 G; 36 T; 0 other;

  Query Match             1.1%;  Score 29.6;  DB 19;  Length 50;
  Best Local Similarity   79.5%;  Pred. No. 5.1e+03;
  Matches   35;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy    2141 AGCCTGCTGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
           || | || | ||  ||||||| |  ||||||||||||||||||
Db       7 AGGCGGCCGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 50

RESULT 10
AAD17216
ID   AAD17216 standard; DNA; 43 BP.
XX
AC   AAD17216;
XX
DT   29-NOV-2001  (first entry)
XX
DE   Human mRNA hybridisation selection reaction biotin-dT3 oligonucleotide.
XX
KW   Human; multiplex ligation-dependent amplification; amplicon;
KW   single nucleotide polymorphism; hybridisation selection reaction; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Biotin-labelled Thymidine"
XX
PN   WO200161033-A2.
XX
PD   23-AUG-2001.
XX
PF   15-FEB-2001; 2001WO-EP01739.
XX
PR   15-FEB-2000; 2000EP-0200506.
XX
PA   (SCHO/) SCHOUTEN J P.
XX
PI   Schouten JP;
XX
DR   WPI; 2001-550053/61.
XX
PT   An improved multiplex ligation-dependent amplification method for
PT   detecting specific single stranded target nucleic acids in samples -
XX
PS   Example 8; Page 137; 158pp; English.
XX
CC   The invention relates to an improved multiplex ligation-dependent
CC   amplification method for detecting specific single stranded target
CC   nucleic acids in samples using a plurality of probe sets comprising at
CC   least 2 probes. Each probe comprises a target specific region and a
CC   non-complementary region comprising a primer binding site. The probes
CC   in each set are ligated when hybridised to a target nucleic acid and
CC   amplified by a primer set. The method is used for detecting a nucleotide
CC   polymorphism, especially a single nucleotide polymorphism; detecting
CC   multiple single stranded target nucleic acid sequences (through the
CC   detection of multiple amplicons); determining the absolute or relative
CC   abundance of multiple single stranded nucleic acids in a sample; and
CC   detection of a break point region in rearranged nucleic acids. By using
CC   a femtomolar amount of the probes, a large number of different probe
CC   sets can be used to simultaneously detect and quantify a corresponding
CC   large number of target sequences with high specificity. The present
CC   DNA sequence is biotin-dT3 labelled fluorescent oligonucleotide which is
CC   used for the hybridisation selection reaction of human mRNA samples.
XX
SQ   Sequence 43 BP; 0 A; 0 C; 0 G; 43 T; 0 other;

  Query Match             1.0%;  Score 29.2;  DB 22;  Length 43;
  Best Local Similarity   81.0%;  Pred. No. 5.9e+03;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;
```

```
Qy    2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
           ||  ||||||| |  ||||||||||||||||||||   |||
Db       1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42
```

RESULT 11
AAV09273/c
ID AAV09273 standard; cDNA; 44 BP.
XX
AC AAV09273;
XX
DT 07-JUL-1998 (first entry)
XX
DE Nucleotide sequence of the 3' portion of the BG513_19 protein.
XX
KW BG513_19 protein; human adult brain cDNA library; nutritional activity;
KW cytokine activity; cell proliferation/differentiation activity;
KW homology; ss.
XX
OS Homo sapiens.
XX
PN WO9748801-A2.
XX
PD 24-DEC-1997.
XX
PF 16-JUN-1997; 97WO-US10501.
XX
PR 17-JUN-1996; 96US-0664596.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Bowman M, Evans C, Jacobs K, LaVallie ER, McCoy JM;
PI Merberg D, Racie LA, Spaulding V, Treacy M;
XX
DR WPI; 1998-063142/06.
XX
PT Poly:nucleotide(s) and proteins obtained from human PBMC, dendritic
PT cell, adult brain, foetal brain and adult testes cDNA libraries -
PT used in research, detection and therapy of, e.g. cytokine and cell
PT proliferation or differentiation
XX
PS Claim 19; Page 51; 78pp; English.
XX
CC This nucleotide sequence encodes the 3' portion of the BG513_19 protein
CC which was isolated from a human adult brain cDNA library. The products
CC of the polynucleotides of the invention can be used in research,
CC detection and therapy, as they may have nutritional activity, cytokine
CC and cell proliferation/differentiation activity. A search against the
CC Genbank database demonstrated that this sequence has no homology
CC with known sequences.
XX
SQ Sequence 44 BP; 44 A; 0 C; 0 G; 0 U; 0 other;

```
  Query Match             1.0%;  Score 29.2;  DB 19;  Length 44;
  Best Local Similarity   81.0%;  Pred. No. 5.9e+03;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy    2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
           ||  ||||||| |  ||||||||||||||||||||   |||
Db      44 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 3
```

RESULT 12
AAT88080/c
ID AAT88080 standard; cDNA; 49 BP.
XX
AC AAT88080;
XX
DT 14-MAY-1998 (first entry)
XX
DE 3' portion of cDNA clone encoding secreted protein AK533.
XX
KW Human; secreted protein; research; treatment; AM533;
KW 3' portion; ds.
XX
OS Homo sapiens.
XX
PN WO9739122-A2.
XX
PD 23-OCT-1997.
XX
PF 11-APR-1997; 97WO-US06042.
XX
PR 12-APR-1996; 96US-0631184.
XX
PA (MURO-) MURO PHARM INC.
XX
PI Theoharides TC;
XX
DR WPI; 1997-526459/48.
XX
PT Human and murine secreted proteins - useful to research or treat
PT diseases or disorders related to their function
XX
PS Disclosure; Page 86; 140pp; English.
XX
CC The present sequence is the 3' portion of a cDNA clone encoding a
CC human secreted protein, which may have nutritional uses, or
CC cytokine and cell proliferation/differentiation, immune stimulating
CC or suppressing, haematopoiesis regulating, tissue growth,
CC activin/inhibin, chemotactic/chemokinetic, haemostatic and
CC thrombolytic, receptor/ligand, anti-inflammatory or tumour
CC inhibition activities. It can also be used to research or treat
CC diseases/disorders related to its function.
CC The partial cDNA clone AP162 was 1st isolated from a human adult
CC placenta cDNA library. The partial cDNA clones AM931, AM610, AM340,
CC AM282, AK647, AK583, AK533 and AK296 were 1st isolated from a human
CC foetal kidney cDNA library. The partial cDNA clones H617 and BB9
CC were 1st isolated from a human peripheral blood monocyte cell (Th1
CC or Th2) cDNA library. The partial cDNA clone AW191 was 1st isolated
CC from a human ovary (PA-1 teratocarcinoma) cDNA library. The partial
CC cDNA clones AT211, AT205 and AT319 were 1st isolated from a human
CC lymphocyte and dendritic cell cDNA library. The partial cDNA clones
CC AS34 and AS32 were 1st isolated from a human foetal brain cDNA
CC library. The partial cDNA clone AR260 was 1st isolated from a human
CC adult retina cDNA library. The partial cDNA clones K640 and K39
CC were 1st isolated from a murine bone marrow (stromal cell line
CC FCM-4) cDNA library.
XX
SQ Sequence 49 BP; 40 A; 2 C; 6 G; 1 T; 0 other;

```
  Query Match             1.0%;  Score 29.2;  DB 18;  Length 49;
  Best Local Similarity   81.0%;  Pred. No. 6.2e+03;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy    2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
           | ||  |||||| |  ||||||||||||||||||||   |||
Db      48 TCGAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 7
```

RESULT 13
AAV02146/c
ID AAV02146 standard; cDNA; 49 BP.
XX
AC AAV02146;
XX
DT 12-MAY-1998 (first entry)
XX
DE Human secreted protein AK533 3' portion including the polyA tail.
XX
KW Human; secreted protein; ATCC 98026; cytokine; immunomodulation;
KW cell proliferation; differentiation; regulation; ds.
XX
OS Homo sapiens.
XX
PN WO9739123-A2.

XX
PD 23-OCT-1997.
XX
PF 14-APR-1997; 97WO-US06139.
XX
PR 18-APR-1996; 96US-0634325.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, Lavallie ER, McCoy JM, Merberg D, Racie LA;
PI Spaulding V;
XX
DR WPI; 1997-526460/48.
XX
PT New secreted proteins encoded clones present in ATCC 98026 -
PT possibly having cytokine, cell proliferation/differentiation
PT regulating, immunomodulating and many other activities
XX
PS Disclosure; Page 86; 139pp; English.
XX
CC The present sequence encodes a portion of a novel human secreted protein
CC deposited under accession number ATCC 98026. The secreted protein can be
CC used to determine biological activity, to raise antibodies, as tissue
CC markers, to isolate cognate ligands or receptors, to identify agents
CC that modulate their interactions and as nutritional supplements. It may
CC also have a very wide range of biological activities although no
CC evidence for any is provided in the specification. Typical of these are
CC cytokine, cell proliferation/differentiation modulating activity or
CC induction of other cytokines; immunostimulating/immunosuppressant
CC activities (e.g. for treating human immunodeficiency virus infection,
CC cancer, autoimmune diseases and allergy); regulation of haematopoiesis
CC (e.g. for treating anaemia or as adjunct to chemotherapy); stimulation
CC of growth of bone, cartilage, tendons, ligaments and/or nerves (e.g. for
CC treating wounds, periodontal disease, neurological diseases stroke,
CC fibrosis); inhibition or stimulation of follicle stimulating hormone
CC (for control of fertility); chemotactic and chemokinetic activities
CC (e.g. for treating infections, tumours); haemostatic or thrombolytic
CC activity (e.g. for treating haemophilia, cardiac infarction etc.);
CC anti-inflammatory activity (e.g. for treating septic shock, Crohn's
CC disease); as antimicrobials; for treating psoriasis or other
CC hyperproliferative disease; for regulation of metabolism, behaviour, and
CC many others. Also contemplated is the use of the corresponding nucleic
CC acid in gene therapy procedures.
XX
SQ Sequence 49 BP; 40 A; 2 C; 6 G; 1 T; 0 other;

Query Match 1.0%; Score 29.2; DB 18; Length 49;
Best Local Similarity 81.0%; Pred. No. 6.2e+03;
Matches 34; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
|| |||||| | |||||||||||||||||||| |||
Db 48 TCGAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 7

RESULT 14
AAQ66922/c
ID AAQ66922 standard; DNA; 50 BP.
XX
AC AAQ66922;
XX
DT 24-JAN-1995 (first entry)
XX
DE Poly-dA 50mer probe target sequence.
XX
KW Target sequence; binding ability; hairpin forming; probes;
KW imperfect hairpin; acceptor label moiety; donor moiety label;
KW fluoresence; fluorophores; specificity; base pair mismatches;
KW competitive arms; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_binding 2..26
FT /*tag= a
FT /note= "Target sequence for probe binding"
XX
PN EP601889-A.
XX
PD 15-JUN-1994.
XX
PF 10-DEC-1993; 93EP-0310007.
XX
PR 10-DEC-1992; 92US-0990298.
XX
PA (MAIN-) MAINE MEDICAL CENT RES INST.
XX
PI Bagwell BC;
XX
DR WPI; 1994-185245/23.
XX
PT Nucleic acid probe for use in DNA or RNA hybridisation assays -
PT comprises a nucleotide sequence which is capable of forming one
PT or more hairpins
XX
PS Disclosure; Fig 2; 25pp; English.
XX
CC This sequence represents a target sequence which was used to demonstrate
CC the binding ability of the hairpin forming probes of the invention. The
CC probes comprise a segment complementary to the target nucleotide and are
CC capable of forming at least 1 imperfect hairpin. The probes contain at
CC least one acceptor label moiety and at least one donor moiety label
CC which are covalently attached to the nucleotide sequence so that when
CC the hairpins are formed the moieties are in close proximity to allow
CC resonance energy transfer between them. This causes a reduction in the
CC fluoresence of the two fluorophores. The target sequence contains at
CC least 22 nucleotides to ensure specificity and avidity of the probe-
CC target hybridisation. The hairpins formed are imperfect hairpins and
CC the intentional base pair mismatches are introduced into the competitive
CC arms such that the specificity sequence will favour binding to the
CC target sequence. Therefore when the probe interacts with the target
CC sequence the competitive arm is displaced, increasing the distance
CC between the fluorophores, resulting in a change in fluorescent emission.
XX
SQ Sequence 50 BP; 50 A; 0 C; 0 G; 0 T; 0 other;

Query Match 1.0%; Score 29.2; DB 15; Length 50;
Best Local Similarity 81.0%; Pred. No. 6.2e+03;
Matches 34; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
|| |||||| | |||||||||||||||||||| |||
Db 50 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 9

RESULT 15
AAF60897/c
ID AAF60897 standard; DNA; 50 BP.
XX
AC AAF60897;
XX
DT 15-MAY-2001 (first entry)
XX
DE Conjugate forming oligonucleotide ON6 SEQ ID 6.
XX
KW Transport; membrane; cytostatic; virucide; vasotropic; dermatological;
KW antipsoriatic; antiasthmatic; gene therapy; tumor cell; antisense;
KW tumor therapy; drug; phosphodiester linkage; ss.
XX
OS Unidentified.
XX
PN DE19935302-A1.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-1999; 99DE-1035302.

XX
PR 28-JUL-1999; 99DE-1035302.
XX
PA (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI Uhlmann E, Greiner B, Unger E, Gothe G, Schwerdel M;
XX
DR WPI; 2001-203679/21.
XX
PT New substituted aryl conjugates of parent molecules, especially
PT oligonucleotides, having improved transmembrane and intracellular
PT transport properties, useful as medicaments or diagnostic agents -
XX
PS Disclosure; Page 9; 28pp; German.
XX
CC This invention describes a novel conjugate (I) which consists of (A) a
CC molecule to be transported and (B) at least one aryl residue of formula
CC -Ar-(X-C(Y)-R_1)_n (II). Ar = group containing at least one aromatic
CC ring; X = O or N (sic); Y = O, S or NH-R_2 (sic); R_1 = optionally
CC substituted 1-23C alkyl (optionally containing double and/or triple
CC bonds); R_2 = optionally substituted 1-18C alkyl (optionally containing
CC double and/or triple bonds); n = integer of 1 or more. (A) is bonded to
CC (B) directly or via a chemical group, provided that the chemical group is
CC other than CH_2-S if the bond is via a phosphodiester linkage of (A). The
CC invention also describes (i) the preparation of a conjugate (I') of (A')
CC a molecule to be transported and (B') at least one aryl residue (not
CC restricted to (II)), by preparing (A') containing a reactive function at
CC the position at which (B') is to be bonded, preparing (B') and reacting
CC (A') and (B'); and (ii) the use of aryl groups (II) (optionally bonded
CC via a chemical group) for transporting (A) across biological membranes.
CC The products of the invention have cytostatic, virucide, vasotropic,
CC dermatological, antipsoriatic and antiasthmatic activity and can be used
CC for gene therapy. Conjugation of (A) with (B) is useful for transporting
CC (A) across biological membranes or into eukaryotic or prokaryotic cells
CC (specifically bacterial, yeast or mammalian cells, including human cells,
CC particularly tumor cells). Medicaments, diagnostic agents and test kits
CC containing (I) are also claimed. Typically (I) are antisense
CC oligonucleotide derivatives for tumor therapy; oligonucleotide drugs for
CC treating viral infections or diseases associated with integrins or
CC cell-cell interactions (e.g. restenosis, vitiligo, psoriasis or asthma);
CC or labeled oligonucleotides for in vivo diagnostic use, e.g. by in situ
CC hybridization. Conjugation with (B) markedly improves the cellular uptake
CC of (A), e.g. in tumor cells. (B) include fluorescein derivative residues,
CC in which case the conjugates (I) are fluorescently labeled, allowing
CC microscopic monitoring of cellular uptake etc. The cellular uptake of (I)
CC is superior to that obtained using other conjugated groups related to
CC (II); e.g. oligonucleotides conjugated with fluorescein diacetate (within
CC the scope of (B)) have superior uptake to corresponding fluorescein
CC conjugates.
XX
SQ Sequence 50 BP; 50 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.0%; Score 29.2; DB 22; Length 50;
Best Local Similarity 81.0%; Pred. No. 6.2e+03;
Matches 34; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
|| ||||||| | |||||||||||||||||||| |||
Db 50 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 9

Search completed: March 3, 2003, 19:29:29
Job time : 598 secs

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 19:18:10 ; Search time 100 Seconds
(without alignments)
8599.216 Million cell updates/sec

Title: US-10-023-782A-3
Perfect score: 2804
Sequence: 1 tcgcagagccgccgatgcgt.....gaaaaaaaaaaaaaaaaaaa 2804

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	29.2	1.0	50	1	US-08-420-443-1	Sequence 1, Appli
	2	28.4	1.0	40	2	US-08-771-624B-1	Sequence 1, Appli
	3	28.4	1.0	40	2	US-08-440-209-4	Sequence 4, Appli
	4	28.4	1.0	40	3	US-08-439-996-4	Sequence 4, Appli
c	5	28.4	1.0	40	4	US-09-732-067-7	Sequence 7, Appli
	6	28	1.0	36	4	US-09-462-569B-4	Sequence 4, Appli
c	7	28	1.0	37	1	US-08-113-646A-44	Sequence 44, Appl
c	8	27.6	1.0	44	1	US-08-664-596B-9	Sequence 9, Appli
	9	27.4	1.0	50	1	US-08-233-609-5	Sequence 5, Appli
	10	27.4	1.0	50	1	US-08-444-083-5	Sequence 5, Appli
	11	27.4	1.0	50	1	US-08-286-304-5	Sequence 5, Appli
	12	27.4	1.0	50	1	US-08-442-745-5	Sequence 5, Appli
	13	27.4	1.0	50	1	US-08-443-129-5	Sequence 5, Appli
	14	27.4	1.0	50	1	US-08-443-952-5	Sequence 5, Appli
	15	27.4	1.0	50	1	US-08-443-130-5	Sequence 5, Appli
	16	27.4	1.0	50	3	US-08-898-911-5	Sequence 5, Appli
	17	27.4	1.0	50	5	PCT-US95-04467-5	Sequence 5, Appli
	18	27.2	1.0	42	1	US-07-875-167-2	Sequence 2, Appli
	19	27.2	1.0	42	1	US-08-287-164-2	Sequence 2, Appli
c	20	27	1.0	47	4	US-09-453-190B-12	Sequence 12, Appl
c	21	27	1.0	47	4	US-09-619-103-10	Sequence 10, Appl
	22	26.8	1.0	41	4	US-09-197-814-9	Sequence 9, Appli
c	23	26.8	1.0	44	1	US-08-113-646A-40	Sequence 40, Appl
	24	26.6	0.9	43	4	US-09-165-239A-5	Sequence 5, Appli
	25	25.8	0.9	45	4	US-08-943-731-657	Sequence 657, App
c	26	25.8	0.9	47	4	US-09-338-907-275	Sequence 275, App
c	27	25.8	0.9	47	4	US-09-218-207-275	Sequence 275, App
	28	25.8	0.9	48	1	US-08-741-881-21	Sequence 21, Appl
	29	25.8	0.9	48	1	US-08-739-158-21	Sequence 21, Appl
	30	25.8	0.9	48	2	US-08-739-167-21	Sequence 21, Appl
	31	25.8	0.9	48	3	US-08-404-796-21	Sequence 21, Appl
	32	25.8	0.9	48	3	US-08-931-869-21	Sequence 21, Appl
	33	25.8	0.9	48	4	US-09-350-399-21	Sequence 21, Appl
	34	25.8	0.9	48	4	US-09-236-140A-21	Sequence 21, Appl
	35	25.8	0.9	50	1	US-08-381-572-20	Sequence 20, Appl
	36	25.8	0.9	50	1	US-08-592-820-20	Sequence 20, Appl
	37	25.6	0.9	33	3	US-09-061-026-26	Sequence 26, Appl
	38	25.6	0.9	33	3	US-09-466-138-26	Sequence 26, Appl
	39	25.6	0.9	40	4	US-09-306-290-27	Sequence 27, Appl
	40	25.6	0.9	47	2	US-08-778-494B-114	Sequence 114, App
	41	25.4	0.9	31	4	US-09-268-505B-13	Sequence 13, Appl
	42	25.4	0.9	47	4	US-09-338-907-275	Sequence 275, App
	43	25.4	0.9	47	4	US-09-218-207-275	Sequence 275, App
c	44	25.2	0.9	30	1	US-08-433-505-9	Sequence 9, Appli
c	45	25.2	0.9	30	3	US-08-870-730-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-08-420-443-1/c
; Sequence 1, Application US/08420443
; Patent No. 5607834
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: C. Bruce Bagwell
; TITLE OF INVENTION: NUCLEIC ACID PROBES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/420,443
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/990,298
; FILING DATE: 19921210
; ATTORNEY/AGENT INFORMATION:
; NAME: Y. Rocky Tsao
; REGISTRATION NUMBER: 34,053
; REFERENCE/DOCKET NUMBER: 05663/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-420-443-1

Query Match 1.0%; Score 29.2; DB 1; Length 50;
Best Local Similarity 81.0%; Pred. No. 5.1e+02;
Matches 34; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
|| ||||||| | |||||||||||||||||||| |||

```
Db      50 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 9


RESULT 2
US-08-771-624B-1
; Sequence 1, Application US/08771624B
; Patent No. 5914230
;  GENERAL INFORMATION:
;    APPLICANT:  Liu, Yen Ping
;    APPLICANT:  Patel, Rajesh D.
;    APPLICANT:  Kurn, Nurith
;    APPLICANT:  Lin, Claire
;    APPLICANT:  Rose, Samuel J.
;    APPLICANT:  Ullman, Edwin F.
;    TITLE OF INVENTION:  Homogeneous Amplification and Detection
;    TITLE OF INVENTION:  of Nucleic Acids
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Behring Diagnostics GmbH, c/o Dade Behring Inc.
;      STREET:  1717 Deerfield Road
;      CITY:  Deerfield
;      STATE:  Illinois
;      COUNTRY:  US
;      ZIP:  60015-0778
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/771,624B
;      FILING DATE:  20-DEC-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/009,090
;      FILING DATE:  22-DEC-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ruszala, Lois K.
;      REGISTRATION NUMBER:  39,074
;      REFERENCE/DOCKET NUMBER:  1030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (847) 267-5364
;      TELEFAX:  (847) 267-6024
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  C-terminal
US-08-771-624B-1

  Query Match             1.0%;  Score 28.4;  DB 2;  Length 40;
  Best Local Similarity   84.2%;  Pred. No. 7e+02;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          ||||||| |  ||||||||||||||||||||   |||
Db      1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 3
US-08-440-209-4
; Sequence 4, Application US/08440209
; Patent No. 5922857
;  GENERAL INFORMATION:
;    APPLICANT:  Han, Jang H
;    APPLICANT:  Spaete, Richard R
;    TITLE OF INVENTION:  Methods and Compositions for Controlling
;    TITLE OF INVENTION:  Translation of HCV Proteins
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield, and Sacks P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/440,209
;      FILING DATE:  12-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/477,895
;      FILING DATE:  06-JUN-1995
;      APPLICATION NUMBER:  US 08/128,583
;      FILING DATE:  28-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Janiuk, Anthony J
;      REGISTRATION NUMBER:  29,809
;      REFERENCE/DOCKET NUMBER:  C0772/7004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
US-08-440-209-4

  Query Match             1.0%;  Score 28.4;  DB 2;  Length 40;
  Best Local Similarity   84.2%;  Pred. No. 7e+02;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          ||||||| |  ||||||||||||||||||||   |||
Db      1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 4
US-08-439-996-4
; Sequence 4, Application US/08439996
; Patent No. 6057093
;  GENERAL INFORMATION:
;    APPLICANT:  Han, Jang H
;    APPLICANT:  Spaete, Richard R
;    TITLE OF INVENTION:  Methods and Compositions for Controlling
;    TITLE OF INVENTION:  Translation of HCV Proteins
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield, and Sacks P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
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;      APPLICATION NUMBER:  US/08/439,996
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,895A
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/128,583
;      FILING DATE:  28-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Janiuk, Anthony J
;      REGISTRATION NUMBER:  29,809
;      REFERENCE/DOCKET NUMBER:  C0772/7004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
US-08-439-996-4

  Query Match             1.0%;  Score 28.4;  DB 3;  Length 40;
  Best Local Similarity   84.2%;  Pred. No. 7e+02;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          ||||||| |  ||||||||||||||||||||   |||
Db      1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 5
US-09-732-067-7/c
; Sequence 7, Application US/09732067
; Patent No. 6457426
; GENERAL INFORMATION:
;  APPLICANT: Ullman, Edwin
;  APPLICANT:  Singh, Rajendra
;  APPLICANT:  DeKeczer, Steve
;  APPLICANT:  Davalian, Dariush
;  TITLE OF INVENTION: Amplified Luminescent Homogeneous
;  TITLE OF INVENTION:  Immunoassay
;  FILE REFERENCE: BEH-7385
;  CURRENT APPLICATION NUMBER: US/09/732,067
;  CURRENT FILING DATE:  2000-12-07
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 40
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: hybridization oligo
US-09-732-067-7

  Query Match             1.0%;  Score 28.4;  DB 4;  Length 40;
  Best Local Similarity   84.2%;  Pred. No. 7e+02;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          ||||||| |  ||||||||||||||||||||   |||
Db     40 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 3


RESULT 6
US-09-462-569B-4
; Sequence 4, Application US/09462569B
; Patent No. 6392124
; GENERAL INFORMATION:
;  APPLICANT: PONZ ASCASO, Fernando
;  APPLICANT:  TORRES PASCUAL, Vicente
;  APPLICANT:  SANCHEZ SANCHEZ, Florentina
;  APPLICANT:  MARTINEZ HERRERA, David
;  TITLE OF INVENTION: INFECTIOUS VECTORS AND CLONES OF PLANTS DERIVED FROM
;  TITLE OF INVENTION:  THE TURNIP MOSAIC VIRUS (TuMV)
;  FILE REFERENCE: P/613-110
;  CURRENT APPLICATION NUMBER: US/09/462,569B
;  CURRENT FILING DATE:  2000-04-03
;  PRIOR APPLICATION NUMBER: PCT/ES98/00200
;  PRIOR FILING DATE: 1998-07-09
;  PRIOR APPLICATION NUMBER: ES P 9701522
;  PRIOR FILING DATE: 1997-07-09
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 36
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: construct
US-09-462-569B-4

  Query Match             1.0%;  Score 28;  DB 4;  Length 36;
  Best Local Similarity   86.1%;  Pred. No. 8.3e+02;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy   2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
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Db      1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 36


RESULT 7
US-08-113-646A-44/c
; Sequence 44, Application US/08113646A
; Patent No. 5578468
;  GENERAL INFORMATION:
;    APPLICANT:  PICKUP, David J.
;    APPLICANT:  PATEL, Dhavalkumar
;    APPLICANT:  ANTCZAK, James B.
;    TITLE OF INVENTION:  SITE-SPECIFIC RNA CLEAVAGE
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VIRGINIA
;      COUNTRY:  U.S.A.
;      ZIP:  22201-4714
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/113,646A
;      FILING DATE:  31-AUG-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/084,406
;      FILING DATE:  10-AUG-1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WILSON, MARY J.
;      REGISTRATION NUMBER:  32,955
;      REFERENCE/DOCKET NUMBER:  1579-20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 816-4000
;      TELEFAX:  (703) 816-4100
;      TELEX:  200797 NIXN UR
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  37 base pairs
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;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA (genomic)
US-08-113-646A-44

  Query Match             1.0%;  Score 28;  DB 1;  Length 37;
  Best Local Similarity   86.1%;  Pred. No. 8.4e+02;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy   2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
          ||  ||||||| |  ||||||||||||||||||||
Db     37 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2

RESULT 8
US-08-664-596B-9/c
; Sequence 9, Application US/08664596B
; Patent No. 5807703
;  GENERAL INFORMATION:
;    APPLICANT:  Jacobs, Kenneth
;    APPLICANT:  McCoy, John
;    APPLICANT:  LaVallie, Edward
;    APPLICANT:  Racie, Lisa
;    APPLICANT:  Merberg, David
;    APPLICANT:  Treacy, Maurice
;    APPLICANT:  Evans, Cheryl
;    APPLICANT:  Spaulding, Vikki
;    APPLICANT:  Bowman, Michael
;    TITLE OF INVENTION:  SECRETED PROTEINS AND POLYNUCLEOTIDES
;    TITLE OF INVENTION:  ENCODING THEM
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc.
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/664,596B
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8224
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  44 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-664-596B-9

  Query Match             1.0%;  Score 27.6;  DB 1;  Length 44;
  Best Local Similarity   78.6%;  Pred. No. 1.1e+03;
  Matches   33;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          ||  ||||||| |  |||||||||||||| |||||   |||
Db     44 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTTTTTTTTTT 3

RESULT 9
US-08-233-609-5
; Sequence 5, Application US/08233609
; Patent No. 5534615
;  GENERAL INFORMATION:
;    APPLICANT:  Baker, Joffre
;    APPLICANT:  Chien, Kenneth
;    APPLICANT:  King, Kathleen
;    APPLICANT:  Pennica, Diane
;    APPLICANT:  Wood, William
;    TITLE OF INVENTION:  Cardiac Hypertrophy Factor and Uses Therefor
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/233,609
;      FILING DATE:  25-APR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  894
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-233-609-5

  Query Match             1.0%;  Score 27.4;  DB 1;  Length 50;
  Best Local Similarity   75.6%;  Pred. No. 1.3e+03;
  Matches   34;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy   2142 GCCTGCTGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
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Db      4 GCCGCGAGCTCGAATTCTTTTTTTTTTTTTTTTTTTTTTTTTTT 48

RESULT 10
US-08-444-083-5
; Sequence 5, Application US/08444083
; Patent No. 5571675
;  GENERAL INFORMATION:
;    APPLICANT:  Baker, Joffre
;    APPLICANT:  Chien, Kenneth
;    APPLICANT:  King, Kathleen
;    APPLICANT:  Pennica, Diane
;    APPLICANT:  Wood, William
;    TITLE OF INVENTION:  Cardiac Hypertrophy Factor and Uses Therefor
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
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;       ZIP:  94080
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  patin (Genentech)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/444,083
;       FILING DATE:  17-MAY-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/233609
;       FILING DATE:  25-APR-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/286304
;       FILING DATE:  05-AUG-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Torchia, Timothy E.
;       REGISTRATION NUMBER:  36,700
;       REFERENCE/DOCKET NUMBER:  894P1D5
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415/225-8674
;       TELEFAX:  415/952-9881
;       TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  50 bases
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-444-083-5

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  Matches   34;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy   2142 GCCTGCTGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTT 2186
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Db      4 GCCGCGAGCTCGAATTCTTTTTTTTTTTTTTTTTTTTTTTTTTT 48


RESULT 11
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; Sequence 5, Application US/08286304
; Patent No. 5571893
;  GENERAL INFORMATION:
;    APPLICANT:  Baker, Joffre
;    APPLICANT:  Chien, Kenneth
;    APPLICANT:  King, Kathleen
;    APPLICANT:  Pennica, Diane
;    APPLICANT:  Wood, William
;    TITLE OF INVENTION:  Cardiac Hypertrophy Factor and Uses Therefor
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/286,304
;      FILING DATE:  05-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/233609
;      FILING DATE:  25-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  894P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-286-304-5

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Db      4 GCCGCGAGCTCGAATTCTTTTTTTTTTTTTTTTTTTTTTTTTTT 48


RESULT 12
US-08-442-745-5
; Sequence 5, Application US/08442745
; Patent No. 5624806
;  GENERAL INFORMATION:
;    APPLICANT:  Baker, Joffre
;    APPLICANT:  Chien, Kenneth
;    APPLICANT:  King, Kathleen
;    APPLICANT:  Pennica, Diane
;    APPLICANT:  Wood, William
;    TITLE OF INVENTION:  Cardiac Hypertrophy Factor and Uses Therefor
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,745
;      FILING DATE:  17-may-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/233609
;      FILING DATE:  25-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/286304
;      FILING DATE:  05-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Torchia, Timothy E.
;      REGISTRATION NUMBER:  36,700
;      REFERENCE/DOCKET NUMBER:  894P1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-8674
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-442-745-5
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  Query Match             1.0%;  Score 27.4;  DB 1;  Length 50;
  Best Local Similarity   75.6%;  Pred. No. 1.3e+03;
  Matches   34;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy   2142 GCCTGCTGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTT 2186
          |||    | | || || ||| |  ||||||||||||||||||||
Db      4 GCCGCGAGCTCGAATTCTTTTTTTTTTTTTTTTTTTTTTTTTTT 48


RESULT 13
US-08-443-129-5
; Sequence 5, Application US/08443129
; Patent No. 5627073
;  GENERAL INFORMATION:
;    APPLICANT:  Baker, Joffre
;    APPLICANT:  Chien, Kenneth
;    APPLICANT:  King, Kathleen
;    APPLICANT:  Pennica, Diane
;    APPLICANT:  Wood, William
;    TITLE OF INVENTION:  Cardiac Hypertrophy Factor and Uses Therefor
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/443,129
;      FILING DATE:  17-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/233609
;      FILING DATE:  25-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/286
;      FILING DATE:  05-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  304
;      FILING DATE:  (null)
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Torchia, Timothy E.
;      REGISTRATION NUMBER:  36,700
;      REFERENCE/DOCKET NUMBER:  894P1D2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-8674
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
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;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
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US-08-443-129-5

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RESULT 14
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; Sequence 5, Application US/08443952
; Patent No. 5679545
;  GENERAL INFORMATION:
;    APPLICANT:  Baker, Joffre
;    APPLICANT:  Chien, Kenneth
;    APPLICANT:  King, Kathleen
;    APPLICANT:  Pennica, Diane
;    APPLICANT:  Wood, William
;    TITLE OF INVENTION:  Cardiac Hypertrophy Factor and Uses Therefor
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
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;      FILING DATE:  17-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/233609
;      FILING DATE:  25-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/286304
;      FILING DATE:  05-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Torchia, Timothy E.
;      REGISTRATION NUMBER:  36,700
;      REFERENCE/DOCKET NUMBER:  894P1D4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-8674
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  5:
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;      TYPE:  nucleic acid
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;      TOPOLOGY:  linear
US-08-443-952-5

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Qy   2142 GCCTGCTGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTT 2186
          |||    | | || || ||| |  ||||||||||||||||||||
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; Sequence 5, Application US/08443130
; Patent No. 5723585
;  GENERAL INFORMATION:
;    APPLICANT:  Baker, Joffre
;    APPLICANT:  Chien, Kenneth
;    APPLICANT:  King, Kathleen
;    APPLICANT:  Pennica, Diane
;    APPLICANT:  Wood, William
;    TITLE OF INVENTION:  Cardiac Hypertrophy Factor and Uses
;    TITLE OF INVENTION:  Therefor
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
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;       STREET:  460 Point San Bruno Blvd
;       CITY:  South San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94080
;     COMPUTER READABLE FORM:
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  patin (Genentech)
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;       FILING DATE:  17-MAY-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/233609
;       FILING DATE:  25-APR-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/286304
;       FILING DATE:  05-AUG-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Torchia, Timothy E.
;       REGISTRATION NUMBER:  36,700
;       REFERENCE/DOCKET NUMBER:  894P1D3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415/225-8674
;       TELEFAX:  415/952-9881
;       TELEX:  910/371-7168
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;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  50 bases
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;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-443-130-5

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Qy   2142 GCCTGCTGATTGATTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
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Db      4 GCCGCGAGCTCGAATTCTTTTTTTTTTTTTTTTTTTTTTTTTT 48


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(without alignments)
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Title: US-10-023-782A-3
Perfect score: 2804
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Gapop 10.0 , Gapext 1.0

Searched: 460893 seqs, 311809382 residues

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Maximum Match 100%
Listing first 45 summaries

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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	30	1.1	45	10	US-09-827-289-18	Sequence 18, Appl
3	29.2	1.0	50	10	US-09-815-343-1012	Sequence 1012, Ap
4	29	1.0	46	10	US-09-827-289-21	Sequence 21, Appl
5	29	1.0	46	10	US-09-827-289-25	Sequence 25, Appl
6	28.4	1.0	46	10	US-09-827-289-22	Sequence 22, Appl
7	28.4	1.0	46	10	US-09-827-289-26	Sequence 26, Appl
c 8	28.2	1.0	36	10	US-09-828-034-3	Sequence 3, Appli
9	27.4	1.0	50	10	US-09-896-856-5	Sequence 5, Appli
c 10	27.2	1.0	36	10	US-09-828-034-2	Sequence 2, Appli
11	27	1.0	44	9	US-10-094-183-9	Sequence 9, Appli
c 12	27	1.0	47	9	US-10-180-819-12	Sequence 12, Appl
c 13	27	1.0	47	9	US-10-208-357-10	Sequence 10, Appl
14	26.8	1.0	41	10	US-09-920-581-9	Sequence 9, Appli
15	26.8	1.0	50	10	US-09-783-590-6670	Sequence 6670, Ap
16	26.6	0.9	45	9	US-09-894-916-3	Sequence 3, Appli
17	26.4	0.9	45	10	US-09-263-959-486	Sequence 486, App
18	26.2	0.9	46	10	US-09-827-289-20	Sequence 20, Appl
19	26.2	0.9	46	10	US-09-827-289-24	Sequence 24, Appl
20	26	0.9	45	10	US-09-827-289-13	Sequence 13, Appl
21	26	0.9	45	10	US-09-827-289-17	Sequence 17, Appl
c 22	25.8	0.9	47	9	US-09-853-526-275	Sequence 275, App
c 23	25.8	0.9	47	10	US-09-901-484A-275	Sequence 275, App
24	25.8	0.9	50	10	US-09-836-077-19	Sequence 19, Appl
c 25	25.4	0.9	46	10	US-09-827-289-21	Sequence 21, Appl
c 26	25.4	0.9	46	10	US-09-827-289-25	Sequence 25, Appl
27	25.4	0.9	47	9	US-09-853-526-275	Sequence 275, App
28	25.4	0.9	47	10	US-09-901-484A-275	Sequence 275, App
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c 30	25.2	0.9	30	9	US-10-042-193A-2	Sequence 2, Appli
c 31	25.2	0.9	40	10	US-09-828-034-1	Sequence 1, Appli
c 32	24.8	0.9	46	10	US-09-827-289-22	Sequence 22, Appl
c 33	24.8	0.9	50	10	US-09-783-590-6670	Sequence 6670, Ap
34	24.6	0.9	33	10	US-09-263-959-825	Sequence 825, App
c 35	24.4	0.9	42	9	US-09-876-235-11	Sequence 11, Appl
c 36	24.4	0.9	42	9	US-09-876-235-12	Sequence 12, Appl
c 37	24.4	0.9	42	9	US-09-876-235-13	Sequence 13, Appl
c 38	24.4	0.9	46	10	US-09-827-289-26	Sequence 26, Appl
c 39	24.4	0.9	48	9	US-09-999-724-14	Sequence 14, Appl
40	24.2	0.9	45	10	US-09-827-289-12	Sequence 12, Appl
41	24.2	0.9	45	10	US-09-827-289-16	Sequence 16, Appl
c 42	24.2	0.9	46	10	US-09-827-289-20	Sequence 20, Appl
c 43	24.2	0.9	47	9	US-09-853-526-198	Sequence 198, App
c 44	24.2	0.9	47	10	US-09-901-484A-198	Sequence 198, App
45	24	0.9	34	10	US-09-923-246-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-09-827-289-14
; Sequence 14, Application US/09827289
; Patent No. US20020009716A1
; GENERAL INFORMATION:
; APPLICANT: Abarzua, Patricio
; TITLE OF INVENTION: Process for Allele Discrimination Using Primer
; TITLE OF INVENTION: Extension
; FILE REFERENCE: 469290-55
; CURRENT APPLICATION NUMBER: US/09/827,289
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194843
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
; OTHER INFORMATION: use in allele discrimination
US-09-827-289-14

Query Match 1.1%; Score 30; DB 10; Length 45;
Best Local Similarity 86.8%; Pred. No. 1e+03;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 18, Application US/09827289
; Patent No. US20020009716A1
; GENERAL INFORMATION:
; APPLICANT: Abarzua, Patricio
; TITLE OF INVENTION: Process for Allele Discrimination Using Primer
; TITLE OF INVENTION: Extension
; FILE REFERENCE: 469290-55

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;  CURRENT APPLICATION NUMBER: US/09/827,289
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: U.S. 60/194843
;  PRIOR FILING DATE: 2000-04-05
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 45
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
;   OTHER INFORMATION: use in allele discrimination
US-09-827-289-18

  Query Match             1.1%;  Score 30;  DB 10;  Length 45;
  Best Local Similarity   86.8%;  Pred. No. 1e+03;
  Matches   33;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy   2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          ||||||| |  |||||||||||||||||||| || ||
Db      4 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCACCTT 41


RESULT 3
US-09-815-343-1012
; Sequence 1012, Application US/09815343
; Patent No. US20010055596A1
; GENERAL INFORMATION:
;  APPLICANT: Meagher, Madeleine
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  King, Gordon E.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.504
;  CURRENT APPLICATION NUMBER: US/09/815,343
;  CURRENT FILING DATE:  2001-03-22
;  NUMBER OF SEQ ID NOS: 1556
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1012
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-815-343-1012

  Query Match             1.0%;  Score 29.2;  DB 10;  Length 50;
  Best Local Similarity   81.0%;  Pred. No. 1.6e+03;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy   2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          ||  ||||||| |  |||||||||||||||||||   |||
Db      1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42


RESULT 4
US-09-827-289-21
; Sequence 21, Application US/09827289
; Patent No. US20020009716A1
; GENERAL INFORMATION:
;  APPLICANT: Abarzua, Patricio
;  TITLE OF INVENTION: Process for Allele Discrimination Using Primer
;  TITLE OF INVENTION:  Extension
;  FILE REFERENCE: 469290-55
;  CURRENT APPLICATION NUMBER: US/09/827,289
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: U.S. 60/194843
;  PRIOR FILING DATE: 2000-04-05
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 46
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
;   OTHER INFORMATION: use in allele discrimination
US-09-827-289-21

  Query Match             1.0%;  Score 29;  DB 10;  Length 46;
  Best Local Similarity   86.5%;  Pred. No. 1.7e+03;
  Matches   32;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy   2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTT 2191
          ||||||| |  |||||||||||||||||||| | ||
Db      1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCATTT 37


RESULT 5
US-09-827-289-25
; Sequence 25, Application US/09827289
; Patent No. US20020009716A1
; GENERAL INFORMATION:
;  APPLICANT: Abarzua, Patricio
;  TITLE OF INVENTION: Process for Allele Discrimination Using Primer
;  TITLE OF INVENTION:  Extension
;  FILE REFERENCE: 469290-55
;  CURRENT APPLICATION NUMBER: US/09/827,289
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: U.S. 60/194843
;  PRIOR FILING DATE: 2000-04-05
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
;   LENGTH: 46
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
;   OTHER INFORMATION: use in allele discrimination
US-09-827-289-25

  Query Match             1.0%;  Score 29;  DB 10;  Length 46;
  Best Local Similarity   86.5%;  Pred. No. 1.7e+03;
  Matches   32;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy   2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTT 2191
          ||||||| |  |||||||||||||||||||| | ||
Db      1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCATTT 37


RESULT 6
US-09-827-289-22
; Sequence 22, Application US/09827289
; Patent No. US20020009716A1
; GENERAL INFORMATION:
;  APPLICANT: Abarzua, Patricio
;  TITLE OF INVENTION: Process for Allele Discrimination Using Primer
;  TITLE OF INVENTION:  Extension
;  FILE REFERENCE: 469290-55
;  CURRENT APPLICATION NUMBER: US/09/827,289
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: U.S. 60/194843
;  PRIOR FILING DATE: 2000-04-05
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 46
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
;   OTHER INFORMATION: use in allele discrimination
US-09-827-289-22

  Query Match             1.0%;  Score 28.4;  DB 10;  Length 46;
  Best Local Similarity   84.2%;  Pred. No. 2.3e+03;
```

```
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          ||||||| |  |||||||||||||||||||  || |
Db      4 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTAT 41


RESULT 7
US-09-827-289-26
; Sequence 26, Application US/09827289
; Patent No. US20020009716A1
; GENERAL INFORMATION:
;  APPLICANT: Abarzua, Patricio
;  TITLE OF INVENTION: Process for Allele Discrimination Using Primer
;  TITLE OF INVENTION:  Extension
;  FILE REFERENCE: 469290-55
;  CURRENT APPLICATION NUMBER: US/09/827,289
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: U.S. 60/194843
;  PRIOR FILING DATE: 2000-04-05
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
;   LENGTH: 46
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
;   OTHER INFORMATION: use in allele discrimination
US-09-827-289-26

  Query Match             1.0%;  Score 28.4;  DB 10;  Length 46;
  Best Local Similarity   84.2%;  Pred. No. 2.3e+03;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          ||||||| |  |||||||||||||||||||  || |
Db      4 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTAT 41


RESULT 8
US-09-828-034-3/c
; Sequence 3, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
;  APPLICANT: Zhong, Weidong
;  APPLICANT:  Hong, Zhi
;  APPLICANT:  Ferrari, Eric
;  TITLE OF INVENTION: HCV REPLICASE COMPLEXES
;  FILE REFERENCE: IN01165
;  CURRENT APPLICATION NUMBER: US/09/828,034
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: U.S. 60/195,852
;  PRIOR FILING DATE: 2000-04-06
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 36
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-3

  Query Match             1.0%;  Score 28.2;  DB 10;  Length 36;
  Best Local Similarity   90.9%;  Pred. No. 2.2e+03;
  Matches   30;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy   2154 ATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
          |||||||| |  ||||||||||||||||||||
Db     36 ATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 4


RESULT 9
US-09-896-856-5
; Sequence 5, Application US/09896856
; Patent No. US20020137189A1
;  GENERAL INFORMATION:
;       APPLICANT: Baker, Joffre
;                  Chien, Kenneth
;                  King, Kathleen
;                  Pennica, Diane
;                  Wood, William
;       TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
;       NUMBER OF SEQUENCES: 8
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 460 Point San Bruno Blvd
;            CITY: South San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/896,856
;            FILING DATE: 29-Jun-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/733,850
;            FILING DATE: 18-OCT-1996
;            APPLICATION NUMBER: US 08/471,112
;            FILING DATE: 06-JUN-1995
;            APPLICATION NUMBER: 08/233,609
;            FILING DATE: 25-APR-1994
;            APPLICATION NUMBER: 08/286304
;            FILING DATE: 05-AUG-1994
;            APPLICATION NUMBER: 08/443129
;            FILING DATE: 17-MAY-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Conley, Deirdre L.
;            REGISTRATION NUMBER: 36,487
;            REFERENCE/DOCKET NUMBER: P0894P1D2C1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415/225-2066
;            TELEFAX: 415/952-9881
;            TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 50 base pairs
;            TYPE: Nucleic Acid
;            STRANDEDNESS: Single
;            TOPOLOGY: Linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-896-856-5

  Query Match             1.0%;  Score 27.4;  DB 10;  Length 50;
  Best Local Similarity   75.6%;  Pred. No. 3.9e+03;
  Matches   34;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy   2142 GCCTGCTGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
          |||    | | || || ||| |  ||||||||||||||||||||
Db      4 GCCGCGAGCTCGAATTCTTTTTTTTTTTTTTTTTTTTTTTTTT 48


RESULT 10
US-09-828-034-2/c
; Sequence 2, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
;  APPLICANT: Zhong, Weidong
;  APPLICANT:  Hong, Zhi
;  APPLICANT:  Ferrari, Eric
```

```
;  TITLE OF INVENTION: HCV REPLICASE COMPLEXES
;  FILE REFERENCE: IN01165
;  CURRENT APPLICATION NUMBER: US/09/828,034
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: U.S. 60/195,852
;  PRIOR FILING DATE: 2000-04-06
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 36
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-2

  Query Match             1.0%;  Score 27.2;  DB 10;  Length 36;
  Best Local Similarity   90.6%;  Pred. No. 3.7e+03;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy   2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
          ||||||| |  |||||||||||||||||||
Db     36 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 5


RESULT 11
US-10-094-183-9
; Sequence 9, Application US/10094183
; Patent No. US20020168631A1
; GENERAL INFORMATION:
;  APPLICANT: Welgene, Inc.
;  TITLE OF INVENTION: Random Gene Unidirectional Antisense Library
;  FILE REFERENCE: 57354.00003
;  CURRENT APPLICATION NUMBER: US/10/094,183
;  CURRENT FILING DATE:  2002-03-08
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 44
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificial Sequence: Synthetic Primer
US-10-094-183-9

  Query Match             1.0%;  Score 27;  DB 9;  Length 44;
  Best Local Similarity   85.7%;  Pred. No. 4.4e+03;
  Matches   30;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy   2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2185
          | || |||||| |  |||||||||||||||||||
Db     10 TCGAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 44


RESULT 12
US-10-180-819-12/c
; Sequence 12, Application US/10180819
; Patent No. US20020177158A1
; GENERAL INFORMATION:
;  APPLICANT: Lohse, Peter
;  APPLICANT:  Kurz, Markus
;  APPLICANT:  Wagner, Richard
;  TITLE OF INVENTION: DNA-PROTEIN FUSIONS AND USES THEREOF
;  FILE REFERENCE: 50036/020002
;  CURRENT APPLICATION NUMBER: US/10/180,819
;  CURRENT FILING DATE:  2002-06-26
;  PRIOR APPLICATION NUMBER: US/09/453,190
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: 60/110,549
;  PRIOR FILING DATE: 1998-12-02
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA linker
US-10-180-819-12

  Query Match             1.0%;  Score 27;  DB 9;  Length 47;
  Best Local Similarity   85.7%;  Pred. No. 4.6e+03;
  Matches   30;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy   2158 TTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          |||| |  |||||||||||||||||| | |||||
Db     45 TTTTTTTTTTTTTTTTTTTTTTTTTTTATCACTTT 11


RESULT 13
US-10-208-357-10/c
; Sequence 10, Application US/10208357
; Publication No. US20020182687A1
; GENERAL INFORMATION:
;  APPLICANT: Kurz, Markus
;  APPLICANT:  Lohse, Peter
;  APPLICANT:  Wagner, Richard
;  TITLE OF INVENTION: Peptide Acceptor Ligation Methods
;  FILE REFERENCE: 50036/031002
;  CURRENT APPLICATION NUMBER: US/10/208,357
;  CURRENT FILING DATE:  2002-07-30
;  PRIOR APPLICATION NUMBER: US/09/619,103
;  PRIOR FILING DATE: 2000-07-19
;  PRIOR APPLICATION NUMBER: 60/145,834
;  PRIOR FILING DATE: 1999-07-27
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: sequence designed to act as a linker
US-10-208-357-10

  Query Match             1.0%;  Score 27;  DB 9;  Length 47;
  Best Local Similarity   85.7%;  Pred. No. 4.6e+03;
  Matches   30;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy   2158 TTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          |||| |  |||||||||||||||||| | |||||
Db     45 TTTTTTTTTTTTTTTTTTTTTTTTTTTATCACTTT 11


RESULT 14
US-09-920-581-9
; Sequence 9, Application US/09920581
; Patent No. US20020151073A1
; GENERAL INFORMATION:
;  APPLICANT: Christensen, Tove
;  TITLE OF INVENTION: A Transcription Factor
;  FILE REFERENCE: 4484.204-US
;  CURRENT APPLICATION NUMBER: US/09/920,581
;  CURRENT FILING DATE:  2001-08-01
;  PRIOR APPLICATION NUMBER: 09/197,814
;  PRIOR FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: PCT/DK97/00305
;  PRIOR FILING DATE: 1997-07-07
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 41
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
```

US-09-920-581-9

Query Match 1.0%; Score 26.8; DB 10; Length 41;
Best Local Similarity 81.6%; Pred. No. 4.7e+03;
Matches 31; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy   2148 TGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2185
          ||   | ||||||| |  ||||||||||||||||||||
Db      4 TGTAAGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 41
```

RESULT 15
US-09-783-590-6670
; Sequence 6670, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6670
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-6670

Query Match 1.0%; Score 26.8; DB 10; Length 50;
Best Local Similarity 81.6%; Pred. No. 5.2e+03;
Matches 31; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy   2164 CCTTTTTTTTTTTTTTTTTTTTTAACTTTGAAAGTTAA 2201
          ||||||||||||||||||||||   ||| |||   ||
Db      9 CCTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAAAAAA 46
```

Search completed: March 3, 2003, 22:38:59
Job time : 180 secs

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 19:09:40 ; Search time 3815 Seconds
(without alignments)
11903.577 Million cell updates/sec

Title: US-10-023-782A-3
Perfect score: 2804
Sequence: 1 tcgcagagccgccgatgcgt.....gaaaaaaaaaaaaaaaaaaa 2804

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	35.2	1.3	49	9	AI270095	AI270095 qt63c08.x
c	2	33.8	1.2	50	9	AA966391	AA966391 w4f01a1.r
c	3	33	1.2	49	9	AA116935	AA116935 mn22g01.r
	4	32.4	1.2	49	9	AI350847	AI350847 qt11e08.x
c	5	31.6	1.1	47	2	HSM002907	Al038431 Homo sapi
c	6	31.4	1.1	50	9	AA120437	AA120437 mn47a11.r
c	7	31.4	1.1	50	9	AA590944	AA590944 vm25f02.r
	8	31.2	1.1	48	10	AV950753	AV950753 AV950753
c	9	31	1.1	46	2	HSM003158	Al038682 Homo sapi
c	10	31	1.1	49	2	HSM001347	Al037023 Homo sapi
	11	31	1.1	49	9	AI431439	AI431439 th36h10.x
c	12	30.8	1.1	45	12	BF582680	BF582680 602094085
c	13	30.8	1.1	47	9	AL642997	AL642997 AL642997
	14	30.8	1.1	47	10	AW250836	AW250836 2821228.3
c	15	30.8	1.1	49	9	AL048743	AL048743 DKFZp566K
	16	30.8	1.1	50	13	BI491716	BI491716 df14b04.w
c	17	30.8	1.1	50	14	BQ256372	BQ256372 NISC_ko01
	18	30.4	1.1	48	9	AL628936	AL628936 AL628936
c	19	30.4	1.1	49	9	AA254893	AA254893 mz78d07.r
	20	30.4	1.1	50	2	HSM009683	Al044833 Homo sapi
	21	30.4	1.1	50	14	BQ393428	BQ393428 NISC_ng03
c	22	30.2	1.1	44	9	AL640163	AL640163 AL640163
	23	30.2	1.1	45	10	AW249952	AW249952 2821663.3
c	24	30.2	1.1	46	2	HSM001086	Al036769 Homo sapi
	25	30.2	1.1	47	2	HSM002960	Al038484 Homo sapi
	26	30.2	1.1	50	9	AL587874	AL587874 AL587874
	27	30	1.1	39	17	TA116F09P	AL462533 T. brucei
	28	30	1.1	49	9	AA526728	AA526728 ni91d10.s
c	29	30	1.1	49	12	BF343486	BF343486 602017592
c	30	30	1.1	49	13	BI090256	BI090256 602855121
c	31	30	1.1	49	13	BI858831	BI858831 603388748
	32	30	1.1	49	17	AZ587341	AZ587341 1M0394O20
c	33	30	1.1	50	2	HSM002946	Al038470 Homo sapi
	34	30	1.1	50	10	AW333255	AW333255 S19D3 AGS
c	35	30	1.1	50	12	BG256941	BG256941 602370419
c	36	30	1.1	50	13	BI493940	BI493940 df106e06.
	37	30	1.1	50	14	BQ265586	BQ265586 NISC_ff07
c	38	29.8	1.1	50	9	AL641164	AL641164 AL641164
	39	29.8	1.1	50	9	AA564185	AA564185 nj04d11.s
c	40	29.6	1.1	36	12	BE894682	BE894682 601435925
	41	29.6	1.1	38	17	AZ773771	AZ773771 2M0001B04
c	42	29.6	1.1	44	12	BG117508	BG117508 602347636
	43	29.6	1.1	45	9	AL587540	AL587540 AL587540
c	44	29.6	1.1	45	12	BF525658	BF525658 602069777
c	45	29.6	1.1	45	17	AZ467950	AZ467950 1M0279L07

ALIGNMENTS

RESULT 1
AI270095
LOCUS AI270095 49 bp mRNA linear EST 17-NOV-1998
DEFINITION qt63c08.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959950 3', mRNA sequence.
ACCESSION AI270095
VERSION AI270095.1 GI:3889262
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 49)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Nan Hu, M.D., Ph.D., Mark Roth, M.D., Phillip Taylor, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.
FEATURES Location/Qualifiers

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     source          1. .49
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1959950"
                     /clone_lib="NCI_CGAP_Eso2"
                     /tissue_type="squamous cell carcinoma"
                     /lab_host="DH10B"
                     /note="Organ: esophagus; Vector: pCMV-SPORT6; Site_1: SalI
                     ; Site_2: NotI; Cloned unidirectionally.  Primer: Oligo
                     dT.  Average insert size 1.1 kb. Life Technologies catalog
                     #: 11502-010"
BASE COUNT        3 a      0 c      2 g     44 t
ORIGIN

  Query Match             1.3%;  Score 35.2;  DB 9;  Length 49;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+05;
  Matches   40;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy    2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTTAACTTTGAAAGT 2198
           ||| ||||||| |  ||||||||||||||||||||    ||| |||||
Db       2 TTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAGT 49


RESULT 2
AA966391/c
LOCUS       AA966391                 50 bp    mRNA    linear   EST 31-JUL-1998
DEFINITION  w4f01a1.r1 Aspergillus nidulans 24hr asexual developmental and
            vegetative cDNA lambda zap library Emericella nidulans cDNA clone
            w4f01a1 5', mRNA sequence.
ACCESSION   AA966391
VERSION     AA966391.1  GI:3140473
KEYWORDS    EST.
SOURCE      Emericella nidulans.
  ORGANISM  Emericella nidulans
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; Emericella.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R.,
            Prade,R. and Roe,B.
  TITLE     An Aspergillus nidulans EST Database
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912
            Fax: 405 325 7762
            Email: broe@ou.edu
            We anticipate the future release of the cDNA clones to the Fungal
            Genetics Stock Center
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Emericella nidulans"
                     /strain="FGSC A26"
                     /db_xref="taxon:162425"
                     /clone="w4f01a1"
                     /clone_lib="Aspergillus nidulans 24hr asexual
                     developmental and vegetative cDNA lambda zap library"
                     /tissue_type="vegetative mycelia, asexual structures"
                     /note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2:
                     XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
                     3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT       42 a      1 c      3 g      4 t
ORIGIN

  Query Match             1.2%;  Score 33.8;  DB 9;  Length 50;
  Best Local Similarity   84.4%;  Pred. No. 5.7e+05;
  Matches   38;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy    2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTTAACTTTGAA 2195
           ||  ||||||| |  ||||||||||||||||||||||||  |||
Db      45 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAACTCCGAA 1


RESULT 3
AA116935/c
LOCUS       AA116935                 49 bp    mRNA    linear   EST 15-NOV-1996
DEFINITION  mn22g01.r1 Beddington mouse embryonic region Mus musculus cDNA
            clone IMAGE:538704 5', mRNA sequence.
ACCESSION   AA116935
VERSION     AA116935.1  GI:1671951
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:325640
            Seq primer: -40m13 ET.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Mus musculus"
                     /strain="C57BL/6 x DBA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:538704"
                     /clone_lib="Beddington mouse embryonic region"
                     /sex="pooled"
                     /tissue_type="embryo"
                     /dev_stage="7.5dpc"
                     /lab_host="DH12S"
                     /note="Organ: whole embryo; Vector: pCMV-SPORT; Site_1:
                     SalI; Site_2: NotI; Cloned unidirectionally.  Primer:
                     Oligo dT. Gastrulating embryos were collected at 7.5dpc
                     from C57BL6 x DBA matings, excluding embryos that had
                     developed head folds and all extraembryonic tissues.
                     Average insert size: 1.3 kb (range: 0.5 - 3.0 kb).
                     Referenced in Development 121, 2479-2489 (1995)"
BASE COUNT       44 a      1 c      0 g      4 t
ORIGIN

  Query Match             1.2%;  Score 33;  DB 9;  Length 49;
  Best Local Similarity   79.6%;  Pred. No. 7.6e+05;
  Matches   39;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy    2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTTAACTTTGAAAGTT 2199
           ||  ||||||| |  ||||||||||||||||||||    ||| |||| |
Db      49 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAGAT 1


RESULT 4
AI350847
LOCUS       AI350847                 49 bp    mRNA    linear   EST 30-DEC-1998
DEFINITION  qt11e08.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1947302 3'
            similar to gb:J05021 EZRIN (HUMAN);, mRNA sequence.
ACCESSION   AI350847
VERSION     AI350847.1  GI:4088053
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
```

```
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1947302"
                     /clone_lib="NCI_CGAP_GC4"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from 3 pooled
                     germ cell tumors, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector.  Library is normalized. Library was constructed by
                     Bento Soares and M. Fatima Bonaldo. "
BASE COUNT        3 a      4 c      3 g     39 t
ORIGIN

  Query Match             1.2%;  Score 32.4;  DB 9;  Length 49;
  Best Local Similarity   85.7%;  Pred. No. 9.3e+05;
  Matches   36;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTTGAAA 2196
           ||||||| |  ||||||||||||||||||||  ||||| ||
Db      1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGCCTTTGCAA 42


RESULT 5
HSM002907/c
ID   HSM002907  standard; RNA; EST; 47 BP.
XX
AC   AL038431;
XX
SV   AL038431.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp566A0246_r1  (from clone DKFZp566A0246)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-47
RA   Ottenwaelder B., Obermaier B., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by MediGenomix within the cDNA
CC   sequencing consortium of the German Genome Project
CC   s1 sequence also available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .47
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp566A0246"
FT                   /clone_lib="566 (synonym: hfkd2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="kidney"
XX
SQ   Sequence 47 BP; 39 A; 1 C; 3 G; 4 T; 0 other;

  Query Match             1.1%;  Score 31.6;  DB 2;  Length 47;
  Best Local Similarity   89.5%;  Pred. No. 1.3e+06;
  Matches   34;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy   2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAA 2188
          ||  |||||||||| |||||||||||||||||||| ||
Db     42 TTTTTTTTTTCTCTTTTTTTTTTTTTTTTTTTCAA 5


RESULT 6
AA120437/c
LOCUS       AA120437                 50 bp    mRNA    linear   EST 19-NOV-1996
DEFINITION  mn47a11.r1 Beddington mouse embryonic region Mus musculus cDNA
            clone IMAGE:541052 5', mRNA sequence.
ACCESSION   AA120437
VERSION     AA120437.1  GI:1675442
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:327988
            Seq primer: -40m13 ET.
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Mus musculus"
                     /strain="C57BL/6 x DBA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:541052"
                     /clone_lib="Beddington mouse embryonic region"
                     /sex="pooled"
                     /tissue_type="embryo"
                     /dev_stage="7.5dpc"
                     /lab_host="DH12S"
                     /note="Organ: whole embryo; Vector: pCMV-SPORT; Site_1:
                     SalI; Site_2: NotI; Cloned unidirectionally.  Primer:
                     Oligo dT. Gastrulating embryos were collected at 7.5dpc
```

from C57BL6 x DBA matings, excluding embryos that had developed head folds and all extraembryonic tissues. Average insert size: 1.3 kb (range: 0.5 - 3.0 kb). Referenced in Development 121, 2479-2489 (1995)"
BASE COUNT 44 a 1 c 1 g 4 t
ORIGIN

Query Match 1.1%; Score 31.4; DB 9; Length 50;
Best Local Similarity 77.6%; Pred. No. 1.3e+06;
Matches 38; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```
Qy   2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTTGAAAGTT 2199
          ||  ||||||| |  ||||||| ||||||||||||   ||| |||| |
Db     50 TTTTTTTTTTTTTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTAAAGAT 2
```

RESULT 7
AA590944/c
LOCUS AA590944 50 bp mRNA linear EST 16-SEP-1997
DEFINITION vm25f02.r1 Knowles Solter mouse blastocyst B1 Mus musculus cDNA clone IMAGE:991227 5', mRNA sequence.
ACCESSION AA590944
VERSION AA590944.1 GI:2404257
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 50)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:563507.
FEATURES Location/Qualifiers
source 1. .50
/organism="Mus musculus"
/strain="C57BL/6J x DBA/2J F1"
/db_xref="taxon:10090"
/clone="IMAGE:991227"
/clone_lib="Knowles Solter mouse blastocyst B1"
/tissue_type="blastocyst"
/dev_stage="embryo (pre-implantation)"
/lab_host="DH10B"
/note="Organ: embryo; Vector: pSPORT; Site_1: NotI; Site_2: SalI; Cloned unidirectionally from mRNA prepared from 800 blastocysts. Primer: SalI(dT): 5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTT-3'. cDNAs were cloned into the NotI/SalI sites of a pSPORT vector (Life Technologies). Two different size selections: B1 (larger inserts) and B3."
BASE COUNT 47 a 1 c 1 g 1 t
ORIGIN

Query Match 1.1%; Score 31.4; DB 9; Length 50;
Best Local Similarity 77.6%; Pred. No. 1.3e+06;
Matches 38; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```
Qy   2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTTGAAAGTT 2199
          ||  ||||||| |  ||||||||||||||||||||   |||||   ||
Db     49 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGATTCTT 1
```

RESULT 8
AV950753
LOCUS AV950753 48 bp mRNA linear EST 14-MAR-2002
DEFINITION AV950753 Nori Satoh unpublished cDNA library, cleavage stage embryo Ciona intestinalis cDNA clone cicl03n20 5', mRNA sequence.
ACCESSION AV950753
VERSION AV950753.1 GI:19439052
KEYWORDS EST.
SOURCE Ciona intestinalis.
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 48)
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES Location/Qualifiers
source 1. .48
/organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone="cicl03n20"
/clone_lib="Nori Satoh unpublished cDNA library, cleavage stage embryo"
/tissue_type="whole animal"
/dev_stage="cleavage stage embryo"
/note="Vector: pBluescript SK"
BASE COUNT 7 a 1 c 3 g 37 t
ORIGIN

Query Match 1.1%; Score 31.2; DB 10; Length 48;
Best Local Similarity 81.8%; Pred. No. 1.4e+06;
Matches 36; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```
Qy   2153 GATTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTTGAAA 2196
          | ||||||| |  ||||||| ||||||||||||   |||||||
Db      1 GGTTTTTTTTTTTTTTTTTCTTTTTTTTTTTTTTTTTTGAAA 44
```

RESULT 9
HSM003158/c
ID HSM003158 standard; RNA; EST; 46 BP.
XX
AC AL038682;
XX
SV AL038682.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp566J2346_r1 (from clone DKFZp566J2346)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-46
RA Ottenwaelder B., Obermaier B., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX

```
CC   Clone from S. Wiemann, sequenced by MediGenomix within the cDNA
CC   sequencing consortium of the German Genome Project
CC   s1 sequence also available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .46
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp566J2346"
FT                   /clone_lib="566 (synonym: hfkd2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="kidney"
XX
SQ   Sequence 46 BP; 41 A; 0 C; 3 G; 2 T; 0 other;

  Query Match             1.1%;  Score 31;  DB 2;  Length 46;
  Best Local Similarity   87.2%;  Pred. No. 1.6e+06;
  Matches   34;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy    2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAAC 2189
           ||  ||||||| | ||||||||||||||||||||| ||
Db      41 TTTTTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTAC 3


RESULT 10
HSM001347/c
ID   HSM001347  standard; RNA; EST; 49 BP.
XX
AC   AL037023;
XX
SV   AL037023.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp564H1864_r1  (from clone DKFZp564H1864)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-49
RA   Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No s1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .49
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp564H1864"
FT                   /clone_lib="564 (synonym: hfbr2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="brain"
XX
SQ   Sequence 49 BP; 39 A; 0 C; 8 G; 2 T; 0 other;

  Query Match             1.1%;  Score 31;  DB 2;  Length 49;
  Best Local Similarity   87.2%;  Pred. No. 1.5e+06;
  Matches   34;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy    2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAAC 2189
           ||  ||||||| | ||||||||||||||||||||| ||
Db      46 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAC 8


RESULT 11
AI431439
LOCUS       AI431439                 49 bp    mRNA    linear   EST 09-MAR-1999
DEFINITION  th36h10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2120419 3'
            similar to contains Alu repetitive element;, mRNA sequence.
ACCESSION   AI431439
VERSION     AI431439.1  GI:4303194
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Life Technologies catalog #: 11548-013
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2120419"
                     /clone_lib="NCI_CGAP_Pan1"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B"
                     /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.72 kb. Life Technologies catalog #:
                     11548-013"
BASE COUNT        4 a      0 c      1 g     44 t
ORIGIN

  Query Match             1.1%;  Score 31;  DB 9;  Length 49;
  Best Local Similarity   78.7%;  Pred. No. 1.5e+06;
  Matches   37;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy    2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTTGAAAG 2197
           ||  ||||||| |  ||||||||||||||||||||    ||| | ||
Db       1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATAG 47


RESULT 12
BF582680/c
LOCUS       BF582680                 45 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  602094085F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4208373 5',
            mRNA sequence.
ACCESSION   BF582680
VERSION     BF582680.1  GI:11656398
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 45)
```

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  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9772  row: j  column: 22
            High quality sequence stop: 45.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4208373"
                     /clone_lib="NCI_CGAP_Co24"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.6 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT       44 a      0 c      1 g      0 t
ORIGIN

  Query Match             1.1%;  Score 30.8;  DB 12;  Length 45;
  Best Local Similarity   83.3%;  Pred. No. 1.7e+06;
  Matches   35;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy   2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          ||  |||||||  |  ||||||||||||||||||||  ||||
Db     44 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTTT 3


RESULT 13
AL642997/c
LOCUS       AL642997                 47 bp    mRNA    linear   EST 12-DEC-2001
DEFINITION  AL642997 XGC-neurula Silurana tropicalis cDNA clone TNeu016o14 5',
            mRNA sequence.
ACCESSION   AL642997
VERSION     AL642997.1  GI:16795122
KEYWORDS    EST.
SOURCE      western clawed frog.
  ORGANISM  Silurana tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Silurana.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (10_2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Huckle E
            Sanger Centre
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TNeu016o14.sp6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="Silurana tropicalis"
                     /db_xref="taxon:8364"
                     /clone="TNeu016o14"
                     /clone_lib="XGC-neurula"
                     /dev_stage="neurula"
                     /lab_host="Escherichia coli DH10B"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from neurula.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
BASE COUNT       46 a      1 c      0 g      0 t
ORIGIN

  Query Match             1.1%;  Score 30.8;  DB 9;  Length 47;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+06;
  Matches   35;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy   2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          ||| |||||||  |  ||||||||||||||||||||  |||
Db     46 TTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 5


RESULT 14
AW250836
LOCUS       AW250836                 47 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821228.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821228 3',
            mRNA sequence.
ACCESSION   AW250836
VERSION     AW250836.1  GI:6593829
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821228.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 40
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 47 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM6  row: E  column: 5
            High quality sequence stop: 40.
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821228"
                     /clone_lib="NIH_MGC_7"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT        3 a      6 c      0 g     38 t
ORIGIN
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  Query Match             1.1%;  Score 30.8;  DB 10;  Length 47;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+06;
  Matches   35;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy   2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTTGAAA 2196
          ||||||| || ||||||||||||||||||||   ||| | |
Db      2 TTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTCACA 43


RESULT 15
AL048743/c
LOCUS       AL048743                 49 bp    mRNA    linear   EST 30-APR-1999
DEFINITION  DKFZp566K163_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
            DKFZp566K163, mRNA sequence.
ACCESSION   AL048743
VERSION     AL048743.1  GI:4727814
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp566K163"
                     /clone_lib="566 (synonym: hfkd2)"
                     /tissue_type="kidney"
                     /dev_stage="fetal"
                     /lab_host="Xl-2blue"
                     /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
BASE COUNT       48 a      0 c      1 g      0 t
ORIGIN

  Query Match             1.1%;  Score 30.8;  DB 9;  Length 49;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+06;
  Matches   35;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy   2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
          ||  ||||||| | ||||||||||||||||||||   |||
Db     45 TTTTTTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTT 4


Search completed: March  3, 2003, 22:33:57
Job time : 3823 secs
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